CCAGGTCCAACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA ${\tt CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC}$ AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCGGCCCACCATGGCCACGCCTGGGC TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCACCACCCGGAGG ${\tt AGGCCACCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT}$ TCTGGTGTTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTTAGGGTGTGTGCT GTCCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCGTGCAGCGTGTGTACCAGCCCTTCC TCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATTTATAGGACCGCCTAC CGCCGCAGCCTGGGCTGGCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAG 🖺 GACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAG GGAGCTGTGTCCAGCCTGCCGCTGCCGCTGCCGGAGGATGGCGGGGTGACACTTGCCAG il. ₱₱ TCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGC CGGCAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG M TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAG m GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCT GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC TCCTGGTGCACTCCTTCCAGCAGCTCGGCCGĆATCGACTCCCTGAGCGAGCAGATTTCCTTC Ų.) LA CTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTC CCACCCTGGCTACCCCCACCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA GCTGAGGGAAGGTACGAGTTCCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC CGGAGGCTGGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAA AGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGT TACAAAT

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC GAAICQPPCRNGGSCVQPGRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCW EGHSLSADGTLCVPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLAS QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

```
Signal sequence:
  amino acids 1-19
  cAMP- and cGMP-dependent protein kinase phosphorylation sites.
  amino acids 93-97, 270-274
N-myristoylation sites.
  amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,
III 191-197, 265-271
U
 Amidation site.
 amino acids 26-30
Aspartic acid and asparagine hydroxylation site.
amino acids 152-164
  Cell attachment sequence.
  amino acids 130-133
  EGF-like domain cysteine pattern signature.
  amino acids 123-135
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GTCAGCCCACGGCGGGGACTATGGTGAAATTCCCGGCGCTCACGCACTACTGGCCCCTGATC CGGTTCTTGGTGCCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCTTGAA CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT ACTCCCTCATGAAGTTCTTCACGGGTCCCATGAGTGACTTCAAAAATGTGGGCCTGGTGTTT GTGAACAGCAAGAGACAGGACCAAAGCCGTCCTGTGTATGGTGGTGGCAGGGGCCATCGC TGCCGTCTTTCACACACTGATAGCTTATAGTGATTTAGGATACTACATTATCAATAAACTGC ACCATGTGGACGAGTCGGTGGGGAGCAAGACGAGAAGGGCCTTCCTGTACCTCGCCGCCTTT CCTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAAACACAAATACAGTTT CCTGGTGGGATGTCCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTTGTAGCCATTTTGC TTCACAGTCACCTGGAATGCCGGGAGCCCCTGCTCATCCCGATCCTCCTTGTACATGGGC GCACTTGTGCGCTGCACCACCCTGTGCCTGGGCTACTACAAGAACATTCACGACATCATCCC GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA CCCTGTGGGTCACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTCG ACAAGAATAACCCCAGCAACAAACTGGTGAGCACGAGCAACACAGTCACGGCAGCCCACATC AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTTGGAC ACCCAACGTGTCTGAGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC TCTGTGTTGTTCCTTTGCGGATCTTCTCCTTCTTCCCAGTTCCAGTCACAGTGAGGGCGCAT CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTCCTTGCCCCCAGCTCTGTGCTGCG GATCATCGTCCTCATCGCCAGCCTCGTGGTCCTACCCTACCTGGGGGTGCACGGTGCGACCC TGGGCGTGGGCTCCTCGCGGGGCTTTGTGGGAGAATCCACCATGGTCGCCATCGCTGCG TGCTATGTCTACCGGAAGCAGAAAAAGAAGATGGAGAATGAGTCGGCCACGGAGGGGGAAGA CTCTGCCATGACAGACATGCCTCCGACAGAGGGGGGGGACATCGTGGAAATGAGAGAGG TTCATACCCCTGCCTCACGAAAACCCAAAAGACACAGCTGCCTCACGGTTGACGTTGTGTCC ■ TCCTCCCCTGGACAATCTCCTCTTGGAACCAAAGGACTGCAGCTGTGCCATCGCGCCTCGGT CACCCTGCACAGCAGGCCACAGACTCTCCTGTCCCCCTTCATCGCTCTTAAGAATCAACAGG TTAAAACTCGGCTTCCTTTGATTTGCTTCCCAGTCACATGGCCGTACAAAGAGATGGAGCCC CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGCAG GAGGCGGTGCACCCCGGAGTCCCCGTTCACACTGAGGAACGGAGACCTGTGAC CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAAATGCCCCGGG GGCAGCAAACTGACATGGTTGAATGATAGCATTTCACTCTGCGTTCTCCTAGATCTGAGCAA GCTGTCAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTTTTAAATTGTCACAAAA CTTTCCTGAAGGTCGCATTAGAGCGAGTCACATGGAGCATCCTAACTTTGCATTTTAGTTTT TACAGTGAACTGAAGCTTTAAGTCTCATCCAGCATTCTAATGCCAGGTTGCTGTAGGGTAAC TTTTGAAGTAGATATTACCTGGTTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTAA TTGAGAATGTACTACGGTACTTCCCTCCCACACCATACGATAAAGCAAGACATTTTATAACG ATACCAGAGTCACTATGTGGTCCTCCCTGAAATAACGCATTCGAAATCCATGCAGTGCAGTA TATTTTTCTAAGTTTTGGAAAGCAGGTTTTTTCCTTTAAAAAAATTATAGACACGGTTCACT AAATTGATTTAGTCAGAATTCCTAGACTGAAAGAACCTAAACAAAAAAATATTTTAAAGATA TAAATATATGCTGTATATGTTATGTAATTTATTTTAGGCTATAATACATTTCCTATTTTCGC ATTTTCAATAAAATGTCTCTAATACAAAAA

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Transmembrane domains:

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374, 408-423, 431-445

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 ${\tt TATTCCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGACACTGAAGAAA}$ ${\tt ACCTTNGTCCTTGCCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT}$ ${\tt CCTACCCTACCTGGGGGTGCACGGTGAGAC}$

GCCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG ${\tt CTGCTGCCCGCCAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCCTCTTCC}$ TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG CCCTGGGTGTGTGAGGAGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGG CTCCCTGCTTGGCTACCGCGTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCT TCTTTTCACCCTGCTCATGCTCTGCGTGAGCAGCCGGGACCCCCGGGCTGCCATCCAG AATGGGTTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACAT TCCTCATCCAGCTGGTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC AAGGCCGAGGAGTGCGATTCCCGTGCCTGGTACGCAGGCCTCTTCTTCTTCACTCTCTT CTACTTGCTGTCGATCGCGGCCGTGGCGCTGATGTTCATGTACTACACTGAGCCCAGCGGCT GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT GCTGTCCTGCCCAAGGTCCAGGACGCCCAACTCGGGTCTGCTGCAGGCCTCGGTCAT CACCCTCTACACCATGTTTGTCACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA ACCCCCATTTGCCAACCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG ACCCAGTGGTGGGATGCCCCGAGCATTGTGGGCCTCATCATCTTCCTCCTGTGCACCCTCTT CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGCCTGTGAGGGCCGGGCC TTTGACAACGAGCAGGACGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCT GGCCTCACTGCACGTCATGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC TACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTGAGGCAGCCT CACAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCT GCCCCTCCCCACACCAATCAGCCAGGCTGAGCCCCCACCCCTGCCCCAGCTCCAGGACCTG CCCCTGAGCCGGGCCTTCTAGTCGTAGTGCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA TGCCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCCTCAGGCTCCACGGGAGCGGG CTGCTGGAGAGCGGGGAACTCCCACCACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTT CCTGGTCACGTCCCCAGGGGACCCTGCCCCCTTCCTGGACTTCGTGCCTTACTGAGTCTCT

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VCVSIAAVLPKVQDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA
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ACEGRAFDNEQDGVTYSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVWVKICAS
WAGLLLYLWTLVAPLLLRNRDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257, 272-283, 324-340, 391-406, 428-444

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><subunit 1 of 1, 285 aa, 1 stop

><MW: 32190, pI: 9.03, NX(S/T): 2

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Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

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GCTGGCGCCGAACC

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGAGCTT
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TAACC

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><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

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Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

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CAGTCACC<u>ATG</u>AAGCTGGGCTGTGTCCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG CTCTGGGTGGCCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGT CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT TCCAGGTCAAGGCCTACACTTTCAGTGAACCCTTCCACCTGATTGTGTCCTATGACTGGCTG ATCCTCCAAGGTCCAGCCAAGCCAGTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC CCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC TGCAGTGGCATCTTCCAGAGCCCTGGTCCTGGGATCCCAGAAACAGCATCTGTTGTGGCTAT CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG CAGGAAGCCCCATGACCTGAGTTGTCAGACAAAGTTGCCCCTGCAGAGGTCAGCTGCCCGC CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCATACTGGTGTGAGGCAGCCACTGAGG ACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT GCTGCACCTCCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAACTGCTCCTGA GGAGGCCCCTGGGCCTCCGCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG CAGGATGTGAGAGTCCTCCTCGGTCACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAGTAAACAGTTCATCCATGATCTCACT TAACCACCCCAATAAATCTGATTCTTTATTTTCTCTTCCTGTCCTGCACATATGCATAAGTA CTTTTACAAGTTGTCCCAGTGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAAATAAATTT ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAA CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCCAGAGGACA TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGGGTTGGGGGATGGTGGGATGT GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG GGCAGTACCCCACAACGAAAAATAATCTGGCCCAAAATGTCAGTTGTACTGAGTTTGAGAAA CCCCAGCCTAATGAAACCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT TATCTCTTTCCAGCCTCATTCAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGCTATG GTCTGTTCTTTAGTTCTAGTTTGTATCCCCTCAAAAGCCATTATGTTGAAATCCTAATCCCC AAGGTGATGGCATTAAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCCTTCCACCAT ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTCGCCAAACACCG ACTCTGTCGTTGCCTTGATCTTGAACTTCCAGCCTCCAGAACTATGAGAAATAAAATTCTGG TTGTTTGTAGCCTAA

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><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

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NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPPTPSSEDPGFSSPL
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

CCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGGGCCACCAGAAGTT TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG ATCTTACTGGGCCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT GGAAGTGCCAGAGAGTGTAACAGGACCTTGGAAAGGGGATGTGAATCTTCCCTGCACCTATG ACCCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCT GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCG CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCCTGGAGATGG ATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGATGGCAACCAAGTCGTG AGAGATAAGATTACTGAGCTCCGTGTCCAGAAACTCTCTGTCTCCAAGCCCACAGTGACAAC TGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC GGGGTTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACCAGGAACCCATC AAAGTAGCAACCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC TGGAGAGACCAGTGCTGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTCGGAAGACATCCCAA ${\tt CAAGAGCATGTCTACGAAGCAGCCAGG} \underline{{\tt TAA}} {\tt GAAGAGTCTCTCCTCTTCCATTTTTGACCCCGT}$ CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAGGGGGGGTGTGGCACAGACCC AATCCTAAGGCCGGAGGCCTTCAGGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT CCAGTGATGAGCCAACTTCCCAGAATCTGGGCAACAACTACTCTGATGAGCCCTGCATAGGA TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTTAAAAATGCCCCATTAGGC CAGGATCTGCTGACATAATTGCCTAGTCAGTCCTTGCCTTCTGCATGGCCTTCTTCCCTGCT ACCTCTCTTCCTGGATAGCCCAAAGTGTCCGCCTACCAACACTGGAGCCGCTGGGAGTCACT GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTTGGCTCTGG GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT TTCTCTTTCTTCAGGGCCAGACAGCTTTTAATTGAAATTGTTATTTCACAGGCCAGGGTTCA ATCATAACAGC

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><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

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VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWYKQQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMT
YPLKATSTVKQSWDWTTDMDGYLGETSAGPGKSLPVFAIILIISLCCMVVFTMAYIMLCRKT
SQQEHVYEAAR

Signal Sequence:

amino acids 1-19

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 282-300

GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCCCAGCTCGCCCGAGGTCCGTCGGA GGCGCCCGGCCCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC GGGATGTCCCTCCTCCTCCTCTTGCTAGTTTCCTACTATGTTGGAACCTTGGGGACTCA CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA GTGGTGATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG AGTGGCCTTTGCTTCCAATTTCCTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTGTGTATT ACTGGCAGCGAATCCGAGAGAAAGAGGGAGGAGGATGAACGTCTGCCTCCCAAATCTAGGATT GACTACAACCACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA CCAGTGCACAGCAGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGT ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT CCTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCCTCCACTCGCTCCACAGCAAAT ${\tt ACGGTC}{\tt TGA}{\tt ATTACAATGGACTTGACTCCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTC}$ TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA GTGAGCATTGCACGGAACAGATTCAGATGAGCATTTTCCTTATACAATACCAAACAAGCAAA AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG AGGTGAATATACCTAAAACTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTCACAATT TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTTCTATGCATTTCTGCAAACTTATTGGATT ATTAGTTATTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC TGAGCTAACCACTTCTAAGAAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC TTCATTTGTCATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAAC TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCCCTCAAAT CAGATGCCTCTAAGGACTTTCCTGCTAGATATTTCTGGAAGGAGAAAATACAACATGTCATT TATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA CCCAACATACCATTATAGTCTCTTCTTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

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><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

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Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

GTCGTTCCTTTGCTCTCCCGCGCCCAGTCCTCCTCGTGTTCTCCTCAGCCGCTGTCGGAGGAGAGCACCCGGA GACGCGGGCTGCAGTCGCGGCGGCTTCTCCCCGCCTGGGCGGCCTCGCCGCTGGGCAGGTGCTGAGCGCCCCTAG GCCCGGGAGGCGCGGTGGATGCGGCGCTGGGCAGAAGCAGCCGCCGATTCCAGCTGCCCCGCGCCCCGGGCG $\tt CCCCTGCGAGTCCCCGGTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCCTGCAGCCGCATC$ GCCCGCCGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCCTGCTTGGATTCCTTAGCACCACACCACAGCTCAG $\tt CCAGAACAGAAGGCCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT$ GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCT GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATG ATTGAGAAATTACCTTGTGCTGCCTTGACTGACCGAGAATGCACTTGCCCACCTGGCATGTTCCAGTCTAACGCT ACCTGTGCCCCCATACGGTGTGTCCTGTGGGTTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCTTCTAGTGTGATGAAATGCAAAGCATACACAGACTGT CTGAGTCAGAACCTGGTGGTGATCAAGCCGGGGACCAAGGAGACAACGTCTGTGGCACACTCCCGTCCTTC TCCAGCTCCACCTTCCCCTGGCACAGCCATCTTTCCACGCCCTGAGCACATGGAAACCCATGAAGTCCCT TCCTCCACTTATGTTCCCAAAGGCATGAACTCAACAGAATCCAACTCTTCTGCCTCTGTTAGACCAAAGGTACTG GCCACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAG CATTTTGACATCAATGAGCATTTGCCCTGGATGATTGTGCTTTTCCTGCTGCTGCTGCTTGTGGTGATTGTGGTG TGCAGTATCCGGAAAAGCTCGAGGACTCTGAAAAAGGGGCCCCGGCAGGATCCCAGTGCCATTGTGGAAAAGGCA GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT AGGGAGGTTGCTGCTTTCTCCAATGGGTACACAGCCGACCACGAGCGGGCCTACGCAGCTCTGCAGCACTGGACC ATCCGGGGCCCCGAGCCAGCCTCGCCCAGCTAATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTTGTGGAG AAGATTCGTGGGCTGATGGAAGACACCACCCAGCTGGAAACTGACAAACTAGCTCTCCCGATGAGCCCCAGCCCG CTTAGCCCGAGCCCCATCCCCAGCCCCAACGCGAAACTTGAGAATTCCGCTCTCCTGACGGTGGAGCCTTCCCCA CAGGACAAGAACAAGGGCTTCTTCGTGGATGAGTCGGAGCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC CCCTGTGACTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTGAAGAG ATTCCCCAGGCTGAGGACAAACTAGACCGGCTATTCGAAATTATTGGAGTCAAGAGCCAGGAGCCAGACC $\tt CTCCTGGACTCTGTTTATAGCCATCTTCCTGACCTGT\underline{A}\underline{G}AACATAGGGATACTGCATTCTGGAAATTACTCA$ GTGTGTGTGTGTGTGTGTGTGTGTTTTAACAGAGAATATGGCCAGTGCTTGAGTTCTTCTCCTTCTC TCTCTCTCTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCCTTTGCCAGGTGTAACTGTTGTGAA ATACCCACCACTAAAGTTTTTTAAGTTCCATATTTTCTCCATTTTTGCCTTCTTATGTATTTTCAAGATTATTCTG TGCACTTTAAATTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCCACACACTGGATTGTGAGGCTCTTAAC TTCTTAAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTCACACCTACTTTTT CCCCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTCATATTCATGG CTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTCACCTGGACACCGTGTAGAATGCTTGATTACTTGTAC $\verb"TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT"$ GACAACTGGGCCACCAAAGAACTTGAACTTCACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTT GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCCAGCTTTGCTTTAAAAGATGTCTTG TTTTTTATATACACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCCTGGTGGGATTCCTTCACCAATT ACTTTAATTAAAAATGGCTGCAACTGTAAGAACCCTTGTCTGATATATTTTGCAACTATGCTCCCATTTACAAATG TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAAGGTGGCGTGGACTCCCTTTGTGTGGGGGGGTTTGTGG AAAAAAAA

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><MW: 71845, pI: 8.22, NX(S/T): 8

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ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRKKGTETEDVRCKQCARGTFSDVPSSVMKC
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHIL
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVVIVVCSIRK
SSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNREKWIYYCNGHGIDILKLVAAQVGSQWKDIY
QFLCNASEREVAAFSNGYTADHERAYAALQHWTIRGPEASLAQLISALRQHRRNDVVEKIRG
LMEDTTQLETDKLALPMSPSPLSPSPIPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLL
RCDSTSSGSSALSRNGSFITKEKKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ
AEDKLDRLFEIIGVKSQEASQTLLDSVYSHLPDLL

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTGGGA CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC C<u>ATG</u>GGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTGGCC TTGATGATTTGAAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG TCACTGCTGCCATTGAAGTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC GAGTACCGCTGTGTCCGGGTGGTCAGAATGCCGTGCTCCAGGTGTTCACAGCTGCTTC GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCCAAC TGGGTTTCCCAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCAGTTC CGGGAGGAGTTTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCAGTGCACAGCCT TGGCCCTGGCAGGCCAGCCTTCAGTTCCAGGGCTACCACCTGTGCGGGGGCTCTGTCATCAC GCCCCTGTGGATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGA CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT GGCCGGGCCACTCACGTTCAATGAATGATCCAGCCTGTGTGCCCTGCCCAACTCTGAAGAGA ACTTCCCCGATGGAAAAGTGTGCTGGACGTCAGGATGGGGGGCCACAGAGGATGGAGGTGAC GCCTCCCTGTCCTGAACCACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCACAG GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG TGGACAGCTGCCAGGGGGACAGCGGGGGGCCCCTGGTGTCAAGAGAGGAGGCTGTGGAAG TTAGTGGGAGCGACCAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC GAGGAAGGGGACAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCGATCCTCCCCT GGACTCCCGTGTAGGAACCTGCACACGAGCAGCACCCTTGGAGCTCTGAGTTCCGGCACCA GTAGCAGGCCCGAAAGAGGCACCCTTCCATCTGATTCCAGCACAACCTTCAAGCTGCTTTTT GTTTTTTGTTTTTTGAGGTGGAGTCTCGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGAAA TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCCTCAGCTTCCCCA GTAGCTGGGACCACAGGTGCCCGCCACCACCCAACTAATTTTTGTATTTTAGTAGAGAC AGGGTTTCACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT CAGCCTCCCACAGTGCTGGGATTACAGGCATGGGCCACGCCTAGCCTCACGCTCCTTTC TGATCTTCACTAAGAACAAAAGAAGCAGCAACTTGCAAGGGCGGCCTTTCCCACTGGTCCAT CTGGTTTTCTCCCAGGGTCTTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCACG TGCAAAGCCACCAACAGCCACTCAGAAAAGACGCACCAGCCCAGAAGTGCAGAACTGCAGTC TTTCACATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAGGCCTATTTTCATGATTTCTT CATTGTCTGGCGTGTCTGCGTGGACTGACGTGAATCAAAATCATCCACTGAAA

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><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

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WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHH
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT
PLWIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAVPLISNKICNHR
DVYGGIISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSFGIGCAEVNKPGVYT
RVTSFLDWIHEQMERDLKT

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

GCCAGAACGGCGCGCGCGCGCACCACACACACGGGGGGAAACTTTTTTAAAAATGAAAGGCTAGAAGA GCTCAGCGGCGCGCGCGCGCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGAAATCCCTCCGGTCGCGA $\tt GCCGGCGACG\underline{ATG}GCAGCGCCCGCTGCCCGTGTCCCCGCCCGCCCCCTCCTGCTCGCCCTGGCCGGTGCTCT$ GCTCGCGCCCTGCGAGGCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTCAGTGCCTCTGT TCGGAGTGGGGACCTCTGGATCCCAGTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGCTGAATATTCGACT CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGT ACGGGGATATTCTGATTCAGCAGTCAGTCTCAGCACGTGTTCTGGTCTCAGGGGGACTTATTGTGTTTGAAAATGA AAGCTATGTCTTAGAACCAATGAAAAGTGCAACCAACAGATACAAACTCTTCCCAGCGAAGAAGCTGAAAAGCGT CCGGGGATCATGTGGATCACATCACAACACCAAACCTCGCTGCAAAGAATGTGTTTCCACCACCCTCTCAGAC ATGGGCAAGAAGGCATAAAAGAGAGACCCTCAAGGCAACTAAGTATGTGGAGCTGGTGATCGTGGCAGACAACCG AGAGTTTCAGAGGCAAGGAAAAGATCTGGAAAAAGTTAAGCAGCGATTAATAGAGATTGCTAATCACGTTGACAA GTTTTACAGACCACTGAACATTCGGATCGTGTTGGTAGGCGTGGAAGTGTGGAATGACATGGACAAATGCTCTGT AAGTCAGGACCCATTCACCAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAATCCCA TGACAATGCGCAGCTTGTCAGTGGGGTTTATTTCCAAGGGACCACCATCGGCATGGCCCCAATCATGAGCATGTG TGAGCTGGGCCACAATTTCGGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA GGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTAACCTGCCGGAAGTCAGGGAGTCTTTCGGGGGCCA GAAGTGTGGGAACAGATTTGTGGAAGAAGGAGGGGGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG CTGCAATGCCACCTGTACCCTGAAGCCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCCAGAGTTCTGCACAGGGGCCAGCCC TCACTGCCCAGCCAATGTGTACCTGCACGATGGGCACTCATGTCAGGATGTGGACGGCTACTGCTACAATGGCAT CTGCCAGACTCACGAGCAGCAGTGTCACGCTCTGGGGACCAGGTGCTAAACCTGCCCCTGGGATCTGCTTTGA GAGAGTCAATTCTGCAGGTGATCCTTATGGCAACTGTGGCAAAGTCTCGAAGAGTTCCTTTGCCAAATGCGAGAT GAGAGATGCTAAATGTGGAAAAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTC CATAGAAACAACATCCCTCTGCAGCAAGGAGGCCGGATTCTGTGCCGGGGGACCCACGTGTACTTGGGCGATGA CATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTGCCTGAATCGTCAATGTCA AAATATTAGTGTCTTTGGGGTTCACGAGTGTGCAATGCAGTGCCACGGCAGAGGGGTGTGCAACAACAGGAAGAA CATCCGGCAAGCAGAAGCAGGAAGCTGCAGAGTCCAACAGGGAGCGCGGCCAGGAGCCCGTGGG ${\tt ATCGCAGGAGCATGCGTCTACTGCCTCACTGACACTCATC} \underline{{\tt TGA}}{\tt GCCCTCCCATGACATGGAGACCGTGACCAGTG}$ CTGCTGCAGAGGAGGTCACGCGTCCCCAAGGCCTCCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT TCCATGACAACAGACACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAA CAGTGCAAGGAAGGCAGCGACTTCCTGGTTGAGCTTCTGCTAAAACATGGACATGCTTCAGTGCTGCTCCTGAG AGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTC TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTTATTATATGAAAAT TGAAACAAACTGGAGAAGAAGGTAGGAGAAAGGGCGGTGAACTCTGGCTCTTTGCTGTGGACATGCGTGACCAGC AGTACTCAGGTTTGAGGGTTTGCAGAAAGCCAGGGAACCCACAGAGTCACCAACCCTTCATTTAACAAGTAAGAA TGTTAAAAAGTGAAAACAATGTAAGAGCCTAACTCCATCCCCCGTGGCCATTACTGCATAAAATAGAGTGCATTT GAAAT

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>< MW: 80177, pI: 7.08, NX(S/T): 5

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YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLA
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGKDLEKVKQRLIEIANHVDKF
YRPLNIRIVLVGVEVWNDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG
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CDCGEPEECMNRCCNATTCTLKPDAVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS
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DDMPDPGLVLAGTKCADGKICLNRQCQNISVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP
FCDKFGFGGSTDSGPIRQAEARQEAAESNRERGQGQEPVGSQEHASTASLTLI

Signal peptide:

amino acids 1-28

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ACAAAACAGTTTTGGGGGTTCAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGA
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GGGCCCAGTGTCCCCTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT
AGTTTTTAATTTATCAGAGACCCTGCCACCCCATTCCATNTCCATCCAAG

CATCCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTTGTATTTTTGGTAGAGATGGGA TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCGCCTCGGCCTCCC AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAAACTTTTTAAGAAGTTAAT GAAACCATACCTTTTACATTTTTAATGACAGGAAAATGCTCACAATAATTGTTAACCCAAAA TTCTGGATACAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAATA TACCAAATATCAATAATACTTATCTCTGGGTAAAAACCTCTTCTCATACCCTGTGCTAACAA CTTTTAACAAAAATTTGCATCACTTTTAAGAATCAAGAAAAATTTCTGAAGGTCATATGGG ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAAGATTCGAAATCTGCCT TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTTGTTTCGA AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCCCC ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAAATGGGTAAGGGGATGGTGGCGA TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTACCCGTGCAGGTTTCTTCATTTGTT CCTTTAACCAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAACAGTGCCCT ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCAT<u>TAA</u>GAGG CAGGTCAAGAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAAATGGTGCCT AGAAGTTCAATGTGGCAAGGAAAAAACCAGGTCTTCATCAAATCTACTAATTTCACTCCTT GACTAGATGATAAATGCCTGTACTCCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG AGGTCAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA AATATTGACTGGGCGTGGTGAGTGCCTGTGATCCCAGCTACTCAGGTGGCTGAAGCAGG ACAATCACTTGAACTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA CACGCCTGTAATCCCGGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA AGACCATCCTGGCTAATACAGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCCGGG GATGGTGGCAGCACCTGGAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATAGCGTGAA CTCAGGAGGCGAGCTTGCAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG

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><subunit 1 of 1, 67 aa, 1 stop

>< MW: 6981, pI: 7.47, NX(S/T): 0

 ${\tt MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVVLLAL}$

LHLYH

Signal peptide:

amino acids 15-27

TGTACACGGCCGACATGTTCACGCACGGGATCCAGAGCGCCGCGCACTTCGTCATGTTCTTCGCGCCCTGGTGTG GACACTGCCAGCGGCTGCAGCCGACTTGGAATGACCTGGGAGACAAATACAACAGCATGGAAGATGCCAAAGTCT ATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCCAGGGGGTGCGAGGATACCCCACCTTAA AGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGGTCCTCGGGACTTCCAGACACTGGAAAACTGGATGC GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAGGCGACCACTTTATCAAGTTCTTCGCTC $\tt CGTGGTGTGGTCACTGCAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCTTGAACATTCCGAAACTG$ TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACTCTGCTCCGGAAACCAGGTTCGTGGCTATCCCACTC TTCTCTGGTTCCGAGATGGGAAAAAGGTGGATCAGTACAAGGGAAAGCGGGATTTGGAGTCACTGAGGGAGTACG TGGAGTCGCAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCACGCCCTCAGAGGCCCCGGTGCTGGCAG TAACCTTCATCAAGTTTTATGCTCCATGGTGTGGTCATTGTAAGACTCTGGCTCCTACTTGGGAGGAACTCTCTA AAAAGGAATTCCCTGGTCTGGCGGGGGTCAAGATCGCCGAAGTAGACTGCACTGCAGCGGAATATCTGCAGCA AGTATTCGGTACGAGGCTACCCCACGTTATTGCTTTTCCGAGGAGGAAAAGTCAGTGAGCACAGTGGAGGCA GAGACCTTGACTCGTTACACCGCTTTGTCCTGAGCCAAGCGAAAGACGAACTTTAGGAACACAGTTGGAGGTCAC CTCTCCTGCCCAGCTCCGCACCCTGCGTTTAGGAGTTCAGTCCCACAGAGGCCACTGGGTTCCCAGTGGTGGCT ATTCTTTATTAAGTTAAGTTCTCTAAGTAAATGTGTAACTCATGGTCACTGTGTAAACATTTTCAGTGGCGATA TATCCCCTTTGACCTTCTCTTGATGAAATTTACATGGTTTCCTTTGAGACTAAAATAGCGTTGAGGGAAATGAAA CCACGAGTTCTGGAAAGGTGGCCTTGTGGCAGTATTGACGTTCCTCTGATCTTAAGGTCACAGTTGACTCAATAC TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACCTCTGGAAGATACCTTCACGGCCGCTGC TGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC GTGCCTGAGTAAGAGAATGCTGATGCCATAACTTTATGTGTCGATACTTGTCAAATCAGTTACTGTTCAGGGGAT CCTTCTGTTTCTCACGGGGTGAAACATGTCTTTAGTTCCTCATGTTAACACGAAGCCAGAGCCCACATGAACTGT TGGATGTCTTCCTTAGAAAGGGTAGGCATGGAAAATTCCACGAGGCTCATTCTCAGTATCTCATTAACTCATTGA AAGATTCCAGTTGTATTTGTCACCTGGGGTGACAAGACCAGACAGGCTTTCCCAGGCCTGGGTATCCAGGGAGGC TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCCTTTTAGAGG CTTGCTATACTTGGTCTGCTTCAAGGAGGTCGACCTTCTAATGTATGAAGAATGGGATGCATTTGATCTCAAGAC CAAAGACAGATGTCAGTGGGCTGTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCCTCTA ACTCATGCTGTCCTTGTGATTAAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCTCTAAGATA CCCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACTGGTGGTAGGAATCTTAGAAACAAGACCACTTATA CTGTCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACCAGCCTCTGCCTTAAAGGAAATCTTTATTAATCACG TATGGTTCACAGATAATTCTTTTTTAAAAAAACCCAACCTCCTAGAGAGCACCACCTGTCAAGAGTCTTGTACA GATACTTTCTAAATAAACTCTTTTTTTTTAA

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><subunit 1 of 1, 432 aa, 1 stop

><MW: 47629, pI: 5.90, NX(S/T): 0

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SDVCSAQGVRGYPTLKLFKPGQEAVKYQGPRDFQTLENWMLQTLNEEPVTPEPEVEPPSAPE
LKQGLYELSASNFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT
QHYELCSGNQVRGYPTLLWFRDGKKVDQYKGKRDLESLREYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL

Signal sequence:

amino acids 1-32

CTTTTCTGAGGAACCACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA CCGCTGAAGTCTGTGCCACACACACACTTTCACCAGGACCCAAAGGAGATGATGGTGAAAAA GGAGATCCAGGAGAAGGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTGGGAAGA AGGGTGACAAAGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACTGGATATTAGTATTGCTCGGCT CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT TCTACTACATCGTGCAGGAAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGG GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACTCATCGCTGACTATGTTGC TGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC CCCTATGGTCATGAGGACTGTGTGGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG $\texttt{CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAG{\textbf{TAA}}\texttt{CTTCCCTCATCCT}$ ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT CCATCATCAAAAAAAAAAAAAAA

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><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

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RKFVGQLDISIARLKTSMKFVKNVIAGIRETEEKFYYIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC
VEMLSSGRWNDTECHLTMYFVCEFIKKKK

Signal peptide:

amino acids 1-25

GGTTCTATCGATTCGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC GCCAGCGCACGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGCCCTAGGTTTT CGGAAGGGAGGATCAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGC GGGCTCCATGGCTGCCTCCTGCTGCTGCCCCTGCTGCTGCTACCGCTGCTGCTGCTGA AGCTACACCTCTGGCCGCAGTTGCGCTGGCTTCCGGCGGACTTGGCCTTTGCGGTGCGAGCT CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCGGAAGG ACACCTTTCTCATTCACGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC AGGGCTGCACGCGCCTTCCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGGCGACAG CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCCGGGAGACCGGAGATGCAGCGGCCG GAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCCGCCCCT CTGTCACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCCAGAGTTTCTGTGGCTCTG GTTCGGGCTGGCCAAGGCCGGCCTGCGCACTGCCTTTGTGCCCACCGCCCTGCGCCGGGGCC CCCTGCTGCACTGCCTCCGCAGCTGCGGCGCGCGCGCGCTGGTGCTGGCGCCAGAGTTTCTG GAGTCCTGGAGCCGGACCTGCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGG GGCCAGTGCCAGGATACCTCTCTCCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTC ACCTCTGGCACCACGGGCCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCCAC TCTACCACATGTCCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCCATTGGGGCCACAGTG GTGCTGAAATCCAAGTTCTCGGCTGGTCAGTTCTGGGAAGATTGCCAGCACACAGGGTGAC GGTGTTCCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACCAGCCCCCGAGCAAGGCAG AACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCCAGATACCTGGGAGCGT TTTGTGCGGCGCTTCGGGCCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT GGCCACCATCAACTACACAGGACAGCGGGGGGCGTTTGGGGGCGTGCTTCCTGGCTTTACAAGC ATATCTTCCCCTTCTCCTTGATTCGCTATGATGTCACCACAGGAGAGCCAATTCGGGACCCC CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCA GCAGTCCCCATTCCTGGGCTATGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGG ATGTCTTCCGGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC CACAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATG GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCTTATGCCCG GCCCCGATTCCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG TTCGGATGGCAAATGAGGGCTTCGACCCCAGCACCCTGTCTGACCCACTGTACGTTCTGGAC CAGGCTGTAGGTGCCTACCTGCCCCTCACAACTGCCCGGTACAGCGCCCTCCTGGCAGGAAA CCTTCGAATC<u>TGA</u>GAACTTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGG CCGTTGCAGGTGTACTGGGCTGTCAGGGATCTTTTCTATACCAGAACTGCGGTCACTATTTT AAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC TTGGCCGCCATGGCCCAACTTGTTTATTGCAG

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><subunit 1 of 1, 730 aa, 1 stop

><MW: 78644, pI: 7.65, NX(S/T): 2

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RAAHTFLIHGSRRFSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERAAPGAGD
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGLAKAGLRTAFVPTAL
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA
EVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP
SKAERGHKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW
LYKHIFPFSLIRYDVTTGEPIRDPQGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPELAQGK
LLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEV
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPPYARPRFLRLQESLATTETFK
QQKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARYSALLAGNLRI

Type II transmembrane domain:

amino acids 45-65

Other transmembrane domain:

amino acids 379-398

cAMP- and cGMP-dependent protein kinase phosphorylation site starting at amino acid 136

CUB domain protein motif

amino acids 254-261

putative AMP-binding domain siganture

amino acids 332-343

N-glycosylation sites

amino acids 37-40 and 483-486

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACCGCGCGCATACACACTCGCTCTC GCTTGTCCATCTCCCTCCCGGGGGGGCCGCGCGCGCCCCCACCTTTGCCGCACACTCCGGC GAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGAACTCGGATTGCAGCTCTGAACCC CCATGGTGGTTTTTTAAACACTTCTTTTCCTTCTCTTCCTCGTTTTGATTGCACCGTTTCCA TCTGGGGGCTAGAGGAGCAGCCAGCCTTCCCAGCCAGCCCTTGTTGGCTTGCCATCGT CCATCTGGCTTATAAAAGTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTCGTCCCCTCGG CTGGCAGAAGGGGTGACGCTGGGCAGCGGGGGGGGGGCGCCGCTGCCTCTGGCGGGCTTT CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTACCGAGCTGGATTTGTATG TTGCACC<u>ATG</u>CCTTCTTGGATCGGGGCTGTGATTCTTCCCCTCTTGGGGCTGCTGCTCTCCC TCCCCGCCGGGGCGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTACGGTGCC AAGGGATTCAGCCTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAGCAAAC TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGG CATAAGAAATTTGACGAATTTTTCCGAGAGCTCCTGGAGAAATGCAGAAAAGTCACTAAATGA TATGTTTGTACGGACCTATGCATGCTGTACATGCAGAATTCAGAAGTCTTCCAGGACCTCT TCACAGAGCTGAAAAGGTACTACACTGGGGGTAATGTGAATCTGGAGGAAATGCTCAATGAC TTTTGGGCTCGGCTCCTGGAACGGATGTTTCAGCTGATAAACCCTCAGTATCACTTCAGTGA AGACTACCTGGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCC GGAAACTGAAGATTCAGGTTACCCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG ACTGTGGGCAGAGTTGCAAACCGAGTTTCCAAGGTCAGCCCAACCCCAGGGTGTATCCG TGCCCTCATGAAGATGCTGTACTGCCCATACTGTCGGGGGCTTCCCACTGTGAGGCCCTGCA ACAACTACTGTCTCAACGTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT TGAGTCGGTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA ACAGCATGCAGGTGTCTGCAAAGGTCTTTCAGGGATGTGGTCAGCCCAAACCTGCTCCAGCC CTCAGATCTGCCCGCTCAGCTCCTGAAAATTTTAATACACGTTTCAGGCCCTACAATCCTGA GGAAAGACCAACAACTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA AATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCCTACACTATCTGCAAGGACGAGAGC GTGACAGCGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT GCCTGAGATCATGAATGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACA TCACTCGGCCTGACACTTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAA CTAAAAAACGCCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG CTCAGGGAGTGGCAGTGCATGGATGACGTGTCCCACGGAGTTTGAGTTTGTCACCA CAGAGGCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCCAGCGTGGC CACTCCCTGCTCCTGGTCTCTCACCTGCATTGTCCTGGCACTGCAGAGACTGTGCAGA<u>TA</u> **A**TCTTGGGTTTTTGGTCAGATGAAACTGCATTTTAGCTATCTGAATGGCCAACTCACTTCTT TTCTTACACTCTTGGACAATGGACCATGCCACAAAAACTTACCGTTTTCTATGAGAAGAGAG CAGTAATGCAATCTGCCTCCCTTTTTGTTTTCCCAAAGAGTACCGGGTGCCAGACTGAACTG CTTCCTCTTTCCTTCAGCTATCTGTGGGGACCTTGTTTATTCTAGAGAGAATTCTTACTCAA ATTTTTCGTACCAGGAGATTTTCTTACCTTCATTTGCTTTATGCTGCAGAAGTAAAGGAAT CTCACGTTGTGAGGGTTTTTTTTTTTTCTCATTTAAAAT

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><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

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EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMF
VRTYGMLYMQNSEVFQDLFTELKRYYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFSEDY
LECVSKYTDQLKPFGDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAERLEGPFNIES
VMDPIDVKISEAIMNMQENSMQVSAKVFQGCGQPKPAPALRSARSAPENFNTRFRPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHSKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMDDVCPTEFEFVTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

Signal peptide:

amino acids 1-23

FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG CAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACTACGCAAAGACCAAGCGGGCTCCGCGGGGACCGGCCGCGGGGC TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT GGAGGGAGATCAGGAAACGGCTTCTTCCTCACTTCGCCGCCTGGTGAGTGTCGGGGAGATTGGCAAACGCCTAGG TCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAGTTCTTTCCAGGTGTGGGGACCGCAGGACAGACGGCCGA TCCCGCCGCCCTCCGTACCAGCACTCCCAGGAGAGTCAGCCTCGCTCCCCAACGTCGAGGGCGCTCTGGCCACGA CGGACATGGTGACAGCTGAGAGGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTCACCGTCTGTTGGGTGCATG GGGGCTGTGCGGGGCATCCGCCTCCGCCTTCTCCACAGGCCTGTGTCTCTGGAAAGATGCTAGCAATGGGGG CGCTGGCAGGATTCTGGATCCTCTCCTCACTTATGGTTACCTGTCCTGGGGCCAGGCCTTAGAAGAGGAGG AAGAAGGGGCCTTACTAGCTCAAGCTGGAGAGAAACTAGAGCCCAGCACAACTTCCACCTCCCAGCCCCATCTCA TTTTCATCCTAGCGGATGATCAGGGATTTAGAGATGTGGGTTACCACGGATCTGAGATTAAAACACCTACTCTTG ACAAGCTCGCTGCCGAAGGAGTTAAACTGGAGAACTACTATGTCCAGCCTATTTGCACACCATCCAGGAGTCAGT TTATTACTGGAAAGTATCAGATACACCCGGACTTCAACATTCTATCATAAGACCTACCCAACCCAACTGTTTAC CTCTGGACAATGCCACCTCAGAAACTGAAGGAGGTTGGATATTCAACGCATATGGTCGGAAAATGGCACT TGGGTTTTAACAGAAAGAATGCATGCCCACCAGAAGAGGATTTGATACCTTTTTTGGTTCCCTTTTTGGGAAGTG GGGATTACTATACACACTACAAATGTGACAGTCCTGGGATGTGTGGCTATGACTTGTATGAAAACGACAATGCTG CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCCATA TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTTCCTGCTTAGATGAAGCAA TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAACAACAGCATTATCATTTACTCTTCAGATAATG GTGGCCAGCCTACGGCAGGAGGAGTAACTGGCCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACTTGTGCACATCACTG ACTGGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT GGGAGACCATAAGTGAGGGTCTTCGCTCACCCCGAGTAGATATTTTGCATAACATTGACCCCTATACACCAAGGC AAAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG GAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCCTCAGTCTTTCAGCAACCTGGGACCGAACCG GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGA GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAAC TGCAGTGCCGGTCAGGTATCCCCCCAAAGACCCCAGAAGTAACCCTAGGCTCAATGGAGGGGTCTGGGGACCATG GAAGAAGAACAGCAGAAAGCAGTCTCAGGTAAACCAGCAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA GGCTTGTTTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCACACTGAAAACTGTCCTGCTCAGTG CCAAGGTGCTACTCTTGCAAGCCACACTTAGAGAGAGTGGAGATGTTTATTTCTCTCGCTCCTTTAGAAAACGTG GTGAGTCCTGAGTTCCACTGCTGTGCTTCAGTCAACTGACCAAACACTGCTTTGAATTATAGGAGGAGAACAATA ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAAACTACCTTTGATAAATTAC

FIGURE 42B

CACATGTGAACAGCTTGCACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCCC ATTTTATTCATTCTTCAAATTATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTCAGACTA ATTACTTGGAAATTCAATGTTTGTGCAGAGTTGAGACAACTTTATTGTTTCTATCATAAACTATTTATGTATCTT AATTATTAAAATGATTTACTTTATGGCACTAGAAAATTTACTGTGGCTTTTCTGATCTAACTTCTAGCTAAAATT GTATCATTGGTCCTAAAAAATAAAAATCTTTACTAATAGGCAATTGAAGGAATGGTTTGCTAACAACCACAGTAA TATAATATGATTTTACAGATAGATGCTTCCCCTTGGCTATGACATGGAGAAAGATTTTCCCATAATAATAACTAA TATTTATATTAGGTTGGTGCAAAACTAGTTGCGGTTTTTCCCATTAAAAGTAATAACCTTACTCTTATACAAAGT ACATGCAAACGTCATGAGGAGAATTAAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTCATCAATGAGCATA GATTGGTGTGGATCCTGTAGACCCTGGTGTTTTCTTTGAAGTGCCCTCTCCTAATGCAGAGGCCTTGAAGCTTAC AGTATACACTTGAAAAGTCACAGATAGCTAGAATTATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGT GGTGGTATGACAGCATACCATTAAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTTATATCAC AACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAATGTATAAAAGAATCTATAAT CTAGTACTGAAATTACTAAATTGGGTAAGATGATTTAAATGATTTTAATTTTTAACATTTTATTTCTAGAATATAT GGCTCCATTTTATTTTATAGTGTAAAGTTGTATTTCCTAAAGTTTGTGTTTTTGTCGACAGTATCTTTTAAATGAG

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><MW: 56885, pI: 6.49, NX(S/T): 5

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SRSQFITGKYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTHMVGKWHLGFNRKEC
MPTRRGFDTFFGSLLGSGDYYTHYKCDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTQRVQQ
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLDEAINNVTLA
LKTYGFYNNSIIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGFVHSPLLKNKGTVCK
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFS
TSQPTHMRGWTYLTGIQES

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGGC CCGTGCGAGAATGCCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTGCTCCTCGGGTGGCAG GTGGTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTTGTTAGCATCGGCACGTCAGCCT GGGGTCTGTCACTATGGAACTAAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG GCAGATGCTTTCCAGGATACACCGGGAAAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTTTTGCCT CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACTCTAGGACATGTGCCATGATAA ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA CTCCGCCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAAATGTCACA ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCCTTCAAGTG TAAATGCAAGCAGGATATAAAGGCAATGGACTTCGGTGTTCTGCTATCCCTGAAAATTCTG AAAAACAGCATGAAAAAGAAGGCAAAAATTAAAAATGTTACCCCAGAACCCACCAGGACTCC TACCCCTAAGGTGAACTTGCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAACT CTCATGGAGGTAAAAAGGGAATGAAGAGAAATGAAAGAGGGGCTTGAGGATGAGAAAAGAG AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTTTTTTCCCT AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAA ACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT GGAAACAGGATAGAGATGATTTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGC CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG ACAAAGTCGGGAAACTTCGAGTGTTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG ACCACGAGTGAGGATGAAAAGTGGAAGACAGGGAAAATTCAGTTGTATCAAGGAACTGATGC TACCAAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGCAAAACCGGCGAAATCGCAGTGG ATGGCGTCTTGCTTCAGGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG TTACTATCTTTATATTTGACTTTGTATGTCAGTTCCCTGGTTTTTTTGATATTGCATCATAG GACCTCTGGCATTTTAGAATTACTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATTG TAAGATGCCTTTCTTGTATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT TCTCAGTCATTTCTGAATCTTTCCNCATTATATATAAAATNTGGAAANGTCAGTTTATCTC CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA GAAAATAGAAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGGA AACTATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC TTGTATATTAATTCTTTGTAATAATAA

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCE
ATCEPGCKFGECVGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGSYKCFCLSGH
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP
YNRRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPTPK
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

Signal peptide:

amino acids 1-21

EGF-like domain cysteine pattern signature. amino acids 80-91

Calcium-binding EGF-like domains amino acids 103-124, 230-251 and 185-206

GGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTCCTGCTCTTGGTGCAGCTGCTG CGCTTCCTGAGGGCTGACGCCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCC AGAATGGGAGCTGACTGAT**ATG**GTGGTGTGGGTGACTGGAGCCTCGAGTGGAATTGGTGAGG AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGTGCTGTCAGCCAGAAGAGTGCAT GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT TGTTTTGCCCCTTGACCTGACCGACACTGGTTCCCCATGAAGCGGCTACCAAAGCTGTTCTCC AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAATGTCCCAGCGTTCTCTGTGC ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTC CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA CTCCGGGGTTTTTTAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA CAAAGACTATAGGCAATAATGGAGACCAGTCCCACAAGATGACAACCAGTCGTTGTGTGCGG CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG GGAAGAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAAATC GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT ATTGCCATGAATCTTGCAAAA

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><subunit 1 of 1, 289 aa, 1 stop

><MW: 32268, pI: 9.21, NX(S/T): 0

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Important Features:

Signal Peptide:

amino acids 1-31

Transmembrane domain:

amino acids 136-157

Tyrosine kinase phosphorylation site.

106-113 and 107-114

Homologous region to Short-chain alcohol dehydrogenase amino acids 80-90, 131-168, 1-13 and 176-185

GCGACGTGGGCACCGCCATCAGCTGTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCTCTGTCC ${\tt TG}{\tt ATG}{\tt CTGCTGGCTGCTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTC}$ TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTCAAGCCGCTCAGCGTGCCTGTG GACAGCGTGGCCCCGGCCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC CTGGGTCCTCACTGCTGCCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGGT CAGTGGTCCTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG GCTGCCTGCAGTTGCCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACTGTATCTACAACCAGCT GCACCAGCGACACCTGTCCAACCCGGCCCGGCCTGGGATGCTATGTGGGGGCCCCCAGCCTG GGGTGCAGGGCCCCTGTCAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGA CACTGGGTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT GCTGCTGACCAACACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGCCAGCTT TCCTGGCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCCTCCCCATGGCCCTGGGAGGCCAGGCT GATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTCAGAGGAGGCGGTGCTAACTG CTGCCCACTGCTTCATTGGGCGCCAGGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGA TCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG GCCCGCCCAGGAGCAGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAG GGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG TGTGTACCAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGTCTGGGGCACCACTGGTG CATGAGGTGAGGGCACATGGTTCCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG CCCCGCCAGGCCGCCGTTCACCGCGCTCCCTGCCTATGAGGACTGGGTCAGCAGTTTGG ACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCGAGGCTGAGCCTGGAAGCTGCCTGGCC AACATAAGCCAACCAGCTGC<u>TGA</u>CAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC AGGCAGGCAAATGGCATTACTGCCCCTGTCCTCCCCACCCTGTCATGTGTGATTCCAGGCAC CTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCCACACCCCAACTCTGCTACCAAGC AAAATAAAA

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PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGA
EEVGVAALQLPRAYNHYSQGSDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTS
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVLC
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERG
WVLGRARPGAGISSLQTVPVTLLGPRACSRLHAAPGGDGSPILPGMVCTSAVGELPSCEGLS
GAPLVHEVRGTWFLAGLHSFGDACQGPARPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEP
GSCLANISQPTSC

Important features:

Signal peptide:

amino acids 1-15

Homologous region to Serine proteases, trypsin family amino acids 79-95, 343-359 and 237-247

N-glycosylation sites.

amino acids 37-40 and 564-567

Kringle domains

amino acids 79-96, 343-360 and 235-247

CGGGCCGCCCCGGCCCCATTCGGGCCGGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGCGCGCGCAGGGGCAGCCTTCCACCACGGGGAG CCCAGCTGTCAGCCGCCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGT GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTCCTTCTCC CCTGAGCCTGGCTCAGCCTGGCACAGCTCATCTGGCAGCTGACAGATACCAAACA GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC GACGAGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCGGCAGCGCTGCCGTCAGCCT GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTC TGGCAGGATGGGCAGGTGTGCCCCTGACTGGCAACGTGACCACGTCGCAGATGGCCAACGA GCAGGGCTTGTTTGATGTGCACAGCGTCCTGCGGGTGGTGCTGCGGAATGGCACCTACA GCTGCCTGGTGCGCAACCCCGTGCTGCAGCAGGATGCGCACRGCTCTGTCACCATCACAGGG TGCACTGCTGGTGGCCCTGGCTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAGGCCTCCAAGACAGCCCTGCAGCCT CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCC<u>TGA</u>CCATGAGGACCAGG GAGCTGCTACCCCTACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTT GCCTTATTTCACAGTACATACATTTCTTAGGGACAGTACACTGACCACATCACCACCCTC TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTCAGA CTGACTGACCCCTGCCTTATTTCACCAAAGACACGATGCATAGTCACCCCGGCCTTGTTTC TCCAATGGCCGTGATACACTAGTGATCATGTTCAGCCCTGCTTCCACCTGCATAGAATCTTT TCTTCTCAGACAGGGACAGTGCGGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCCTTTC CCCTCCTTCCTCCCCGAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG AGGGGACTGCCCCCACCCCACCATGGTGCTATTCTGGGGCTGGGGCAGTCTTTTCCTGGC TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG GATGTCATCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC AAAAAAAAAAA

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><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

>< MW: -1, pI: 4.62, NX(S/T): 4

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LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGVPL
TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA
LWVTVGLSVCLIALLVALAFVCWRKIKQSCEEENAGAEDQDGEGEGSKTALQPLKHSDSKED
DGQEIA

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC amino acids 217-234

TTCGTGACCCTTGAGAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC CTGAACTTGTCTGAAGCCCTTGTCCGTAAGCCTTGAACTACGTTCTTAAATCTATGAAGTCG AGGGACCTTTCGCTGCTTTTGTAGGGACTTCTTTCCTTGCTTCAGCAACATGAGGCTTTTCT TGTGGAACGCGGTCTTGACTCTGTTCGTCACTTCTTTGATTGGGGCCTTTGATCCCTGAACCA GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTCATCTGCCATCGCAAGACCAAAGGAGGGGGA TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC ACAAACATAACAATGGTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT TCTGGGCTATGGAAAAGAAGGAAAAGGTAAAATTCCCCCAGAAAGTACACTGATATTTAATA TTGATCTCCTGGAGATTCGAAATGGACCAAGATCCCATGAATCATTCCAAGAAATGGATCTT AATGATGACTGGAAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA ACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTGATAAAG AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA TAGAGATACATCTACCCTTTTAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAA GGGAAGAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTTCACTTTCACAG ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAAATGTTGCAACTGGGAATATACC ACGACATGAGACCAGGTTATAGCACAAATTAGCACCCTATATTTCTGCTTCCCTCTATTTTC TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT GTTATAATGAAATAGTTTATGTGTAACTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAG GCTGAGGCGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCCTGTAATCCCAGCT ACCCAGGAAGGCTGAGGCGGCAGATCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAG ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAGAACACGGTTAATACCATATNA ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGAT TGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC TAGCGGAATATCCTTCCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA TTGTATCATAAGATAAAGTAGTAAACCAGTCTACATTTTCCCATTTCTGTCTCAACAAAC TGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGGGGCCAAGGAGGG TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTA CTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCCAGCTACTCGGGAG GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

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><subunit 1 of 1, 211 aa, 1 stop

><MW: 24172, pI: 5.99, NX(S/T): 1

MRLFLWNAVLTLFVTSLIGALIPEPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSL FHSTHKHNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPEST LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVED IFDKEDEDKDGFISAREFTYKHDEL

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

CCAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCCTCTCCCGTAGCCCACCCGA CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT CACGGGGCTCAGTCTCTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTAC CTGCCACCTCAACGTCCTCAATGGCTCTGACGCCCGCCTGCCCTGCACCTTCAACTCCTGC TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACTGCTC TGAGGAGATGTTCCTCCAGTTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAG ACCGCGTGGAGTTCTCAGGGAACCCCAGCAAGTACGATGTCGGTGATGCTGAGAAACGTG CAGCCGGAGGATGAGGGGATTTACAACTGCTACATCATGAACCCCCCTGACCGCCACCGTGG CCATGGCAAGATCCATCTGCAGGTCCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG GTCAAGTGTGAGGAGAAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA CTCTTGGTGTGCTTCCCGTGACCTAGGACCCCAGGGCCCACCTGGGGCCTCCTGAACCCCCG ACTTCGTATCTCCCACCCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA TGCTCTGGGACGTGTGGGCCCTGGGGAGAGAGAGAGAGGCTCCCACCTGCCAGTCCCTGG GGAGGGCCGCTGTCACCTGCCCAGTGCTTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGG GGAGGGAGGGCTTTCCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTG TGCTCCTCCCTGCTCCCAGCCCAGAGCAGCCATCAGGCTGAGGTGACGATGAGTTCCTGA AACTTGGAGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGG CTGCAGGCAAAGCTGGACATGTGCCCTGGCCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCCAGCGGGGACCCACCAACAGAGGCC AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCAG GCTCTGCCTTCTCCATGGGGTAACCACCCTCGCCTGGGCAGGGGGAGCCAAGGCTGGGAAAT GAGGAGGCCATGCACAGGGTGGGGCAGCTTTCTTTGGGGCTTCAGTGAGAACTCTCCCAGTT GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAAGGCCTGAGGCCG GCATAAGGGGAGGCCTTGGAACCTGAGCTGCCAATGCCAGCCCTGTCCCATCTGCGGCCACG CTACTCGCTCCCCAACAACTCCCTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC ACAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGGATTACCTCCAT CTGTTTAGTAGAAATGGGCAAAACCCCATCTCTACTAAAAATACAAGAATTAGCTGGGCGTG GTGGCGTGTGCCTGTAATCCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG GGAAGCAGAGGTTGCAGTGAACTGAGATAGTGATAGTGCCACTGCAATTCAGCCTGGGTGAC ATAGAGAGACTCCATCTCAAAAAAAA

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<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

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Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA
GTTCTCGCCCCCCCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTT
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC
TCAATGGCTCTGACGCCCGCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACACTGCTCTGAGGAGATGTTCCTCCAG
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG
GAACCCCAGCAAGTACGATGTTCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA
TTTACAACTGCTACATCATGAACCCCCC

 $\tt TGCGGCGACCGTCGTACACC{\color{blue}\underline{\textbf{ATG}}} GGCCTCCACCTCCGCCCCTACCGTGTGGGGCTGCTCCCGGATGGCCTCCTGT$ CTGGTGATTTGGGTAACCAACTGGAAGCCAAGCTGGACAAGCCGACAGTGGTGCACTACCTCTGCTCCAAGAAGA CCGAAAGCTACTTCACAATCTGGCTGAACCTGGAACTGCTGCTGCTGTCATCATTGACTGCTGGATTGACAATA TCAGGCTGGTTTACAACAAAACATCCAGGGCCACCCAGTTTCCTGATGGTGTGGATGTACGTGTCCCTGGCTTTG GGAAGACCTTCTCACTGGAGTTCCTGGACCCCAGCAAAAGCAGCGTGGGTTCCTATTTCCACACCATGGTGGAGA GCCTTGTGGGCTGGGGCTACACACGGGGTGAGGATGTCCGAGGGGCTCCCTATGACTGGCGCCGAGCCCCAAATG AAAACGGGCCCTACTTCCTGGCCCTCCGCGAGATGATCGAGGAGATGTACCAGCTGTATGGGGGCCCCGTGGTGC TGGTTGCCCACAGTATGGGCAACATGTACACGCTCTACTTTCTGCAGCGGCAGCCGCAGGCCTGGAAGGACAAGT ACAACAACCGGATCCCAGTCATCGGGCCCCTGAAGATCCGGGAGCAGCAGCGGTCAGCTGTCTCCACCAGCTGGC TGCTGCCCTACAACTACACATGGTCACCTGAGAAGGTGTTCGTGCAGACACCCACAATCAACTACACACTGCGGG AAGCCACGATGCCACCTGGCGTGCAGCTGCACTGCCTCTATGGTACTGGCGTCCCCACACCAGACTCCTTCTACT ATGAGAGCTTCCCTGACCGTGACCCTAAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACTTGAAGAGTGCCC TGCAGTGCCAGGCCTGGCAGAGCCGCCAGGAGCACCAAGTGTTGCTGCAGGAGCTGCCAGGCAGCGAGCACATCG AGATGCTGGCCAACGCCACCACCCTGGCCTATCTGAAACGTGTGCTCCTTGGGCCC<u>TGA</u>CTCCTGTGCCACAGGA CTCCTGTGGCTCGGCCGTGGACCTGCTGTTGGCCTCTGGGGCTGTCATGGCCCACGCGTTTTGCAAAGTTTGTGA GTGGCAGTGAAGAAGAAGAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAATGCTGCTGATGGTGGA TGTCCCCCTATTCCTGTGGGCTTTTCATACTTGCCTACTGGGCCCTGGCCCCGCAGCCTTCCTATGAGGGATGTT GCCACAGATAGGCCTGCCACTGGTCATGGGTAGCTAGAGCTGCTTGCCTTGTGGCTTAGCTGGTCGCCAGCC CCTGGGACATCTCACTCCACTCCCTACCTCCCTTACCACCAGGAGCATTCAAGCTCTGGATTGGGCAGCAGATGTG CTCCCTTCACCCTGGGACTGTGGTTCCAAGGATGAGAGCAGGGGTTGGAGCCATGGCCTTCTGGGAACCTATGGA GAAAGGGAATCCAAGGAAGCAGCCAAGGCTGCTCGCAGCTTCCCTGAGCTGCACCTCTTGCTAACCCCACCATCA CACTGCCACCCTGCCCTAGGGTCTCACTAGTACCAAGTGGGTCAGCACAGGGCTGAGGATGGGGCTCCTATCCAC CCTGGCCAGCACCCAGCTTAGTGCTGGGACTAGCCCAGAAACTTGAATGGGACCCTGAGAGAGCCAGGGGTCCCC TGAGGCCCCCTAGGGGCTTTCTGTCTGCCCCAGGGTGCTCCATGGATCTCCCTGTGGCAGCAGGCATGGAGAGT CAGGGCTGCCTTCATGGCAGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCGAGAAAAGGGTACAGCCTCTAGGT GGGGTTCCCAAAGACGCCTTCAGGCTGGACTGAGCTGCTCTCCCACAGGGTTTCTGTGCAGCTGGATTTTCTCTG TTGCATACATGCCTGGCATCTGTCTCCCCTTGTTCCTGAGTGGCCCCACATGGGGCTCTGAGCAGGCTGTATCTG

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><MW: 46658, pI: 6.65, NX(S/T): 4

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YLCSKKTESYFTIWLNLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDVRVPGFGKTFSL
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEEMYQ
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI
PVIGPLKIREQQRSAVSTSWLLPYNYTWSPEKVFVQTPTINYTLRDYRKFFQDIGFEDGWLM
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLLGP

Important features:

Signal peptide:

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

CGGACGCGTGGGCGGCGGCGCGCGCGCGCGCGACATGGAGAGCGG GCCTACGGCGCCCAAGGCGGCCGCCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA GGTGGTGCGCGCGCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTG AGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCCGGCCTTCTTCTTGGT GGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTTGGTTTCTGCTTCCTCACCAAC CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCAT CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT GCCTACGCCTCCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAA CGCGGAGACCACCGAGGGCTACCAGCCGCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAA GGGGGACAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAACTGCCA GCCCCTCTCTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCCTCGCTTTTAATGA CCTCAGCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT CAGCTTCCCCCGGCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCA CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGGCCACCACCCTGTGCCGGT GGCCTCTGGGCTGCCTCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTG CTCCCACCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTC TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTC TGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACG GAATAAATGTTTTCTCATTCAAAG

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304</pre>

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

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Important features:

Type II Transmembrane domain:

amino acids 1-45

Other transmembrane domains:

amino acids 74-90, 108-126 and 145-161

N-glycosylation site.

amino acids 97-100

GAGCCACCTACCCTGCTCCGAGGCCAGGCCTCCAGGGCCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG CCCGTGGCCGAGGCCCCCAGGTGGCTGGCGGGCAGGGGACGAGGTGATGGCGAGGAGCCAGAGGGG ATGTTCAAGGCCTGTGAGGACTCCAAGAGAAAAGCCCGGGGCTACCTCCGCCTGGTGCCCCTGTTTGTGCTGCTG GCCCTGCTCGTGCTTCGGCGGGGGTGCTACTCTGGTATTTCCTAGGGTACAAGGCGGAGGTGATGGTCAGC CAGGTGTACTCAGGCAGTCTGCGTGTACTCAATCGCCACTTCTCCCAGGATCTTACCCGCCGGGAATCTAGTGCC TTCCGCAGTGAAACCGCCAAAGCCCAGAAGATGCTCAAGGAGCTCATCACCAGCACCCGCCTGGGAACTTACTAC AACTCCAGCTCCGTCTATTCCTTTGGGGAGGGACCCCTCACCTGCTTCTTCTGGTTCATTCTCCAAATCCCCGAG CACCGCCGGCTGATGCTGAGCCCCGAGGTGGTGCAGGCACTGCTGGTGGAGGAGCTGCTGTCCACAGTCAACAGC TCGGCTGCCGTCCCCTACAGGGCCGAGTACGAAGTGGACCCCGAGGGCCTAGTGATCCTGGAAGCCAGTGTGAAA GACATAGCTGCATTGAATTCCACGCTGGGTTGTTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCCTCCGGCTG AAGGGGCCTGACCACCTGGCCTCCAGCTGCCTGTGGCACCTGCAGGGCCCCAAGGACCTCATGCTCAAACTCCGG ATCACCTCGGTGTACGGCTGCAGCCGCCAGGAGCCCGTGGTGGAGGTTCTGGCGTCGGGGGCCATCATGGCGGTC GTCTGGAAGAAGGGCCTGCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCCAGGCCTGT GAAGTGAACCTGACGCTGGACAACAGGCTCGACTCCCAGGGCGTCCTCAGCACCCCGTACTTCCCCAGCTACTAC TCGCCCCAAACCCACTGCTCCTGGCACCTCACGGTGCCCTCTCTGGACTACGGCTTGGCCCTCTGGTTTGATGCC TATGCACTGAGGAGGCAGAAGTATGATTTGCCGTGCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGT GGCTTGCGCATCCTGCAGCCCTACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACC TCCCAGATCTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAACCAGTCGGACCCCTGCCCTGGA GAGTTCCTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGACTGCCCCAACGGCCTGGAT GAGAGAAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGACACATGCATCTCACTGCCCAAGGTCTGT GATGGGCAGCCTGATTGTCTCAACGGCAGCGATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCACC TTCCAGTGTGAGGACCGGAGCTGCGTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCCGACTGCAGGGACGGC TCGGATGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGTCCTCCGAG GGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCGGGGGTCGACACATCTGTGGGGGGGCCCTCATCGCTGACCGC TGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCATGGCCTCCACGGTGCTGTGGACCGTGTTCCTGGGC AAGGTGTGGCAGAACTCGCGCTGGCCTGGAGAGGTGTCCTTCAAGGTGAGCCGCCTGCTCCTGCACCGTACCAC GAAGAGGACAGCCATGACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCGCTCGGCCGCCGTGCGC CCCGTCTGCCTGCCCGCGCGCTCCCACTTCTTCGAGCCCGGCCTGCACTGCTGGATTACGGGCTGGGGCGCCTTG CGCGAGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTGATCCCACAGGACCTGTGCAGCGAG GCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGCCGGCTACCGCAAGGGCAAGAAGGATGCCTGTCAGGGT GACTCAGGTGGTCCGCTGGTGTGCAAGGCACTCAGTGGCCGCTGGTTCCTGGCGGGGCTGGTCAGCTGGGGCCTG GGCTGTGGCCGGCCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGTG ACC<u>TGA</u>GGAACTGCCCCCTGCAAAGCAGGGCCCACCTCCTGGACTCAGAGAGCCCAGGGCAACTGCCAAGCAGG CTGATGTCTGCTCCAGTGATGGCAGGAGGATGGAGAAGTGCCAGCAGCTGGGGGTCAAGACGTCCCCTGAGGACC GCAGTGGCTCAGCAGCAAGAATGCTGGTTCTACATCCCGAGGAGTGTCTGAGGTGCGCCCCACTCTGTACAGAGG GGAAGGTGCTCCCATCGGAGGGGACCCTCAGAGCCCTGGAGACTGCCAGGTGGGCCTGCTGCCACTGTAAGCCAA

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152</pre>

><subunit 1 of 1, 802 aa, 1 stop

><MW: 88846, pI: 6.41, NX(S/T): 7

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YYNSSSVYSFGEGPLTCFFWFILQIPEHRRLMLSPEVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGQVLRLKGPDHLASSCLWHLQGPKDLML
KLRLEWTLAECRDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY
YDPFVLSVQPVVFQACEVNLTLDNRLDSQGVLSTPYFPSYYSPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPCTQGQWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS
LPKVCDGQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKKPNPQCDGRPDCRDGSDEEHCD
CGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIADRWVITAAHCFQEDSMASTVL
WTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG
KKDACQGDSGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIOOVVT

Important features:

Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447 and 509-512

Kringle domains.

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779 ·

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT CTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAACCAGTCGGACCCCTGCC TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGA CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCACCTTCCAGTGTGAGGACCGG AGCTGCGTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCCGACTGCAGGGACGGCTCGGA TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCGGGGTCGACACATCTGTGGG GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT GGCCTCCACGGTGCTGTGGACCGTGTTCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG GAGAGGTGTCCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT GACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCGCTCGGCCGCCGTGCGCCC CGTCTGCCTGCCCGCGCTCCCACTTCTTCGAGCCCGGCCTGCACTGCTGGATTACGGGCT GGGGCGCCTTGEGCGAGGGCGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG ATCCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC CGGCTACCGCAAGGGCAAGAAGGATGCCTGTCAGGGTGACTCAGGTGGTCCGCTGGTGTGCA ${\tt AGGCACTCAGTGGCCGGTTCCTGGCGGGGCTGGTCAGCTGGGCCTGGGCCTGGGCCGGGCCTGGGCCGGGGCCTGGGCCGGGGCCTGGGCCGGGGCCTGGGCCGGGGCCTGGGCCGGGGCCTGGGCCCGGGCCCGGCCCGGGCCC$ CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT GACCTGAGGAACTGCCCCCTGCAAAGCAGGGCCCACCTCCTGGACTCAGAGAGCCCAGGGC AACTGCCAAGCAGGGGGACAAGTAT

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG CTCCGTGCCGCCAAGTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCCAGCCCCTGGCCG ACTTCTGTTTCTTGGGAGGGGTGTGGCGGGGCAGGATGAGCAACTCCGTTCCTCTGCTCTG TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG TTTAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTCGGCCACAG CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTCATCATTCACGGAT GGACGATGAGCGGTATCTTTGAAAACTGGCTGCACAAACTCGTGTCAGCCCTGCACACAAGA GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCACCAGCTTTACACGGA TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG AGAAGGACGATTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGC CGGGCCCATGTTTGAAGGGGCCGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTG TGGATGTCCTCCACACCTACACGCGTTCCTTCGGCTTGAGCATTGGTATTCAGATGCCTGTG TCCACCTCTTTGTTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTGCCTTCCAGTGCACT GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG CAGGCATGCCTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCA CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGCATGTCCTAGGAAAGGGAATCTTT AAAAAAAAAAAAAAAAAAAA

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><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

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PLAHQLYTDAVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV
GRITGLDPAGPMFEGADIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLVNQDKPSFAFQCTDSNRFKKGICLS
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

Important features:

Signal peptide:

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

CGGCAAAGTTTGGCCCGAAGAGGGAAGTGGTCTCAAACCCCGGCAGGTGGCGACCAGGCCAGACCAGGGGGCGCTCG $\tt CTGCCTGCGGGGGCTGTAGGCGAGGGCGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG$ AGAAGAGTGCGGCGGCGGACGGAAAAACAACTCCAAAGTTGGCGAAAGGCACCGCCCCTACTCCCGGGCTGCCG CCGCCTCCCCGCCCCAGCCCTGGCATCCAGAGTACGGGTCGAGCCCGGGCCATGGAGCCCCCCTGGGGAGGCGG CACCAGGAGCCTGGGCGCCGGGGCTCCGCGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCTTCCG ${\tt GCACCTCTGGACAGCCCAGG} \underline{{\tt ATG}} {\tt CTGTTGGCCACCCTCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG}$ ACCGGATTATTTTCCAAATCATGCTTGTGAGGACCCCCCAGCAGTGCTCTTAGAAGTGCAGGGCACCTTACAGA TGATCTCCCTGTGTGAGGCACCTCCCAGCCCTCTGCAGCTGCCCGGGGGGCAACGTCACCATCACTTACAGCTATG CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCCTGCTCTACAGCCAAGATTGGCTGATGTGCCTGCAGGAAG AGTTTCAGTGCCTGAACCACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCTGTGGCGATGGCT TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCTGGATATACACACCTAGCCTCAGTCTCCCACCCCAGT CCTGCCATTGGCTGCACCCCCATGATGGCCGGCGGCTGGCCGTTCACAGCCCTGGACTTGGGCTTTG GAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCCTGAGAGCTCCCGACTACTGCGTAGTCTCACCCACTTCA GCAATGCCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCCTACCACACAGTTGCTTGGAGCA $\tt CTGGCCTGGGAGCCGAAGGCCTAGGTGAGCGCTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACT$ GTGCTGACGGCACAGATGAGGAGGACTGCCCAGGCTGCCCACCTGGACACTTCCCCTGTGGGGCTGCTGGCACCT CTGGTGCCACAGCCTGCTACCTGCTGACCGCTGCAACTACCAGACTTTCTGTGCTGATGGAGCAGATGAGA GACGCTGTCGGCATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCGTGTATGAGACGTGGGTGTGCG ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTCATTACAG TTCGCACCCAGGAGTACAGCATCTTTGCCCCCCTCTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGCACCCC CTTCCTACGGGCAGCTCATTGCCCAGGGTGCCATCCCACCTGTAGAAGACTTTCCTACAGAGAATCCTAATGATA ACTCAGTGCTGGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCCAGGTG CCAACACCCCGGCTCGGGCCTCTGAGGCCAGATCCCAGGTCACACCTTCTGCTGCTCCCCTTGAGGCCCTAGATG AGGCTCCCCTCCCATCTGCTAGCACGTCTCCAGCCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC TGCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGCAGGCCCTGCGAGGCCGCCTGTTGCCCAGCCTGGGGCCCC CAGGACCAACCCGGAGCCCCCTGGACCCCACACAGCAGTCCTGGCCCTGGAAGATGAGGACGATGTGCTACTGG TGCCACTGGCTGAGCCGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGG ${\tt ACCACTTCCTTGCCTGGATTTCAGGGACTTGGTGGGCCTCCCGTTGACCCTATGTAGCTGCTATAAAGT}$ TAAGTGTCCCTCAGGCAGGGAGAGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCCAGTCCCT TCACCACCACCTGCTCCCCACGCCACCACTTTGGGTGGCTGTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA GGTCTGGACACTCCATCCTTGCCAAACCTCTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAACTAGAGA $\tt CCCTCCAGCCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTTGCCATCCACAATCCCTCCTACAGGGCCTGG$ CTCACAAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA **GGAATCATACATCTC**

</usr/segdb2/sst/DNA/Dnasegs.min/ss.DNA49631</pre>

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

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Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins amino acids 411-431, 152-171, 331-350 and 374-393

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645

><subunit 1 of 1, 152 aa, 1 stop

><MW: 17170, pI: 9.62, NX(S/T): 1

MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTFFIIAQAPEPYIVITGFEVTVILFFILL YVLRLDRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTLTVGGGVFALVTAVCCLAD GALIYRKLLFNPSGPYQKKPVHEKKEVL

Important features:

Potential type II transmembrane domain:

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

GGGCGAGAAGTAGGGGAGGCGTGTTCCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTTTATNATCGCACAAGCCCC
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATACTTTTAT
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TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTNTTGCCGAC

CAGCCCGCGCGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG CTCTGCTGGCCCAGTGGCTCCTGCGCGCCCCGGAGCTGGCCCCCGCGCCCCTTCACGCTG CCCCTCCGGGTGGCCGCGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCC TGCCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC CTGGAGATGCTGATCGGGACCCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAA CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTTGCCTGGGATTAAATGGAATGGAATAC ${\tt TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC}$ CTGGTGACACAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG AAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC CATCGTGGACAGTGGCACCACGCTGCTGCGCCCAGAAGGTGTTTGATGCGGTGGTGG AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG CTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT GAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTCAGC CCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTCGGCATTTCCCCCATCCACAAAT GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAA GAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG CCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT AATCGTCCTGCTGCTGCCGTTCCGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTCGTCA ATGATGAGTCCTCTCGGTCAGACATCGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAA CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG CTTTCTCCTGTGCCCACCCGTCTTCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATTCAC TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA AAAAAAACTTCATTCTAA

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><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

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Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

 $\tt CGCCTCCGCCTTCGGAGGCTGACGCCCCGGGCCCCGTTCCAGGCCTGTGCAGGGCGGATCG$ ${\tt GGC} \underline{\textbf{ATG}} {\tt GAGGCGCTGCTGGGCGCGGGGGTTGCTGCTGGGGCGCTTACGTGTCTACTA}$ TCACGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCGGGGAGCG GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC ${\tt GGTATCAGTTCCTGTGGCCGGACCCGTGAGGCGTTTAACCTGCTGCTTCGGGTGAACCATAT}$ ${\tt TGGTGGTGGTAGCCTCAGCTGCCCACTGTCGGGGACGTCTTGACTTCAAACGCCTGGACCGC}$ $\tt CCAGTGGTGGCTGCGGCAGGAGCTGCGGCTAATGCTGACACTAAGCTGGCTAATGTACT$ GTTTGCCCGGGAGCTCGCCAACCAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCCACC CAGGGCCTGTGAACTCGGAGCTGTTCCTGCGCCATGTTCCTGGATGGCTGCGCCCACTTTTG CGCCCATTGGCTGGTGCTCCGGGCACCAAGAGGGGGTGCCCAGACACCCCTGTATTG TGCTCTACAAGAGGGCATCGAGCCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGGAAG AGGTGCCTCCAGCTGCCCGAGACGACCGGCCAGCCATCGGCTATGGGAGGCCAGCAAGAGG $\tt CTGGCAGGGCTTGGGGGGGGGGTGCTGAACCCGATGAAGACCCCCAGTCTGAGGACTC$ AGAGGCCCCATCTTCTCTAAGCACCCCCCCCCCTGAGGAGCCCACAGTTTCTCAACCTTACC CCAGCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG $\texttt{CCTGAGATCCAGCTCTCC} \underline{\textbf{TAA}} \\ \texttt{CCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCTT} \\$ GAAAACCTCGGATGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCCTGGTTGAAGGAAT AATGGGTGATTATTTCTTCCTGAGAGTGACAGTAACCCCAGATGGAGAGATAGGGGTATGCT AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATTCTG ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG TGAACTGATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCCATGTTAATGAAGCG ${\tt GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGGGGCCTG}$ GGATCTGAACCCAAGGGTCTGAGGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA GTCAGGGCAGCAGCTGGTATCGAGGTGCCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG ATGCAGGGCTGGGGTCATCTGTATCTGAAGCCCCTCGGAATAAAGCGCGTTGACCGCCAAAA AAAAAAAAAAAAA

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227</pre>

<subunit 1 of 1, 377 aa, 1 stop</pre>

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSGIGKMTALELARRGAR VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG ISSCGRTREAFNLLLRVNHIGPFLLTHLLLPCLKACAPSRVVVVASAAHCRGRLDFKRLDRP VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPVNSELFLRHVPGWLRPLLR PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDDRAAHRLWEASKRL AGLGPGEDAEPDEDPQSEDSEAPSSLSTPHPEEPTVSQPYPSPQSSPDLSKMTHRIQAKVEP EIQLS

Important features:

Signal peptide:

amino acids 1-16

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

 ${\tt CAAGCCTCAGGCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCTGAGCATGGTGCCCCCAGAC}$ CCACACCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCACGATGGCCAG GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGCGCT ${\tt TTTACTCTGGAATGTGGGCCCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTG}$ CAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTCAGCTGGAAAATGTGACACTGCTGAACCCGGAT CGGGCTCGAGGCCCTGACACCTGCTGCTCCTGAGGCTGCCGGAAAAAGTGCCCAGTGCCCCACCTCAGGAA $\tt GTGACTCTAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCCACCACCTGCTGAAAACCACAATGGCATC$ ${\tt ACCCAGCTGGAAATCGCCACCCATATGCCAGGCTCCTACTGCGTGCAAGTGGCTGCAGTCACTGGTGCTGGAGCT}$ ${\tt GGTCCCTGGACCCTGGAGCAGCTGAGGCTACCTTGAAGCGGCCTGAGGTCATTGCCACCTGCGGTGTTGCACTC}$ ${\tt TGGCTGCTTCTGGGCACCGCCGTGTGTATCCACCGCCGGCGCCGAGCTAGGGTGCACCTGGGCCCAGGTCTG}$ GACCCACTAGACTGTCGTCGCTCCTTGCTCTCCTGGGACTCCCGAAGCCCCGGCGTGCCCCTGCTTCCAGACACC $\tt GTCAGGCGCCTCCCACCCCAGCTGGCCCAGCTCTCCAGCCCCTGTTCCAGCTCAGACAGCCTCTGCAGCCGCAGG$ ${\tt GGACTCTCTTCTCCCCGCTTGTCTCTGGCCCCTGCAGAGGCTTGGAAGGCCAAAAAGAAGCAGGAGCTGCAGCAT}$ ${\tt GCCAACAGTTCCCCACTGCTCCGGGGCAGCCACTCCTTGGAGCTCCGGGCCTGTGAGTTAGGAAATAGAGGTTCC}$ GGGTACATCAGCGTCCCAACAGCCTCAGAGTTCACGGACATGGGCAGGACTGGAGGAGGGGTGGGGCCCAAGGGG GGAGTCTTGCTGTGCCCACCTCGGCCCTGCCTCACCCCCACCCCAGCGAGGGCTCCTTAGCCAATGGTTGGGGC GCTCACTTTGCCCGGGCCCTGGCAGTGGCTGTGGATAGCTTTGGTTTCGGTCTAGAGCCCAGGGAGGCAGACTGC GTCTTCATAGATGCCTCATCACCTCCCTCCCCACGGGATGAGATCTTCCTGACCCCCAACCTCTCCCTGCCCCTG ${\tt TGGCCCCTGACTCTCAGATCTCTTCCCAGAGAAGTCAGCTCCACTGTCGTATGCCCAAGGCTGGTGCTTCTCCT}$ TTCTCCCTCCACGATTGTGAAAACAAATGAAAACAAAATTAGAGCAAAGCTGACCTGGAGCCCTCAGGGAGCAAA ACATCATCTCCACCTGACTCCTAGCCACTGCTTTCTCCTCTGTGCCATCCACTCCCACCACGACCAGGTTGTTTTGGC $\tt CTGAGGAGCAGCCTGCTGCTCTTCCCCCACCATTTGGATCACAGGAAGTGGAGGAGCCAGAGGTGCCTTT$ $\tt GTGGAGGACAGCAGTGGCTGGGAGAGGGCTGTGGAGGAGGAGGGTTCTCGGAGCCCCTCTCAGCCTTACCT$ TATGAGACCGTAGGTCAAAAGCACCATCCTCGTACTGTTGTCACTATGAGCTTAAGAAATTTGATACCATAAAAT GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404</pre>

<subunit 1 of 1, 985 aa, 1 stop

<MW: 105336, pI: 6.55, NX(S/T): 7

MGGMAQDSPPQILVHPQDQLFQGPGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHHLLP DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEKSDEGTYMCV ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLLNPDPAEGPKPRPAVWLSWKV SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG PDSNVLLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYOVWSLGNTSLPP ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPW TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST FYGSLIAELPSSTPARPSPOVPAVRRLPPOLAOLSSPCSSSDSLCSRRGLSSPRLSLAPAEA WKAKKKQELQHANSSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS SSNELVTRHLPPAPLFPHETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPPSPQASS LSGPSPASSRLSSSSLSSLGEDODSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY GYISVPTASEFTDMGRTGGGVGPKGGVLLCPPRPCLTPTPSEGSLANGWGSASEDNAASARA SLVSSSDGSFLADAHFARALAVAVDSFGFGLEPREADCVFIDASSPPSPRDEIFLTPNLSLP LWEWRPDWLEDMEVSHTQRLGRGMPPWPPDSQISSORSOLHCRMPKAGASPVDYS

Important features:

Transmembrane domain:

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

CTCCCACGGTGTCCAGCGCCCAGA**ATG**CGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCT CCCAGGTTATGAAGCCCTGGAGGGCCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT GGGATCCTCTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGA ACCTCACCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG TCTTTACTGATCTCTGTTCGTCTTTCCAGGACCCTGCTGTCCTCCCCTCCCCTTCTCCCAC CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCC CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG GCTGAGGCCCCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCATGCAGC TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCCTGGTGCTGAGCCTTCTGTCAGC CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCC CCTTCCCAGGCCCCTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA GCTGGGCTTCTCGAAGTTTGTCTCAGCG<u>TAG</u>GGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCCTCCCAGGCTCTCCTCTTGCATGTTCCA GCCTGACCTAGAAGCGTTTGTCAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG GAGACTGGGACATCCCTGATAGGTTCACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACTCCTGGGC TGGCGTCCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT GTGAAAAACGTGATTCCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG GACTCTGAATTCTAACAATGCCCAGTGACTGTCGCACTTGAGTTTGAGGGCCAGTGGGCCTG ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCC CAATAGATCTGCTCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCTGCTAAG TCCAGGCCTTGGTCAGGTCAGGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCCTTTGGAAAAAATGATGAAGA AAACCTTGGCTCCTTGTCTGGAAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA GAAAAGTAGAAAACCAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTCGGGGGTGGTGGTAAAGTA GCACAACTACTATTTTTTTTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCGCCTCCTGGGTTCAAGTGATT TTTGTACTTTTAGTAGAGATGGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACTCCTGAC CTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG TCTGGCCCTATTTCCTTTAAAAAGTGAAATTAAGAGTTGTTCAGTATGCAAAACTTGGAAAG ATGGAGGAGAAAAGGAAAAGGAAGAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT TATTTCGTTTTGTTGTACTTCCTTCCACTCTTTTCTTCACATAATTTGCCGGTGTTCTT TTTACAGAGCAATTATCTTGTATACAACTTTGTATCCTGCCTTTTCCACCTTATCGTTCC GCTGCATAAAAAAAAAAAAA

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196</pre>

<subunit 1 of 1, 332 aa, 1 stop</pre>

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSIRDSRQELSLIVTLWNLTLQDAGEYWCGVEKRGPDESLLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAEEKEAPSQAPEGD
VISMPPLHTSEEELGFSKFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA GCCGCAGAGCCAGAGCAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA GCCTGTTCTCTCTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAA AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG TCAGCTGCCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG CTACATGACTTCGGGCTGGACGGATACCGGGGGTACAGCCTGGCTGACTGGCTTGC TTATTTCACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCCCAAC GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCC AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA CAGCAGGCTGGGAAATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA AAGGATGGTTGAACGTGAAA

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187
<subunit 1 of 1, 146 aa, 1 stop
<MW: 16430, pI: 5.05, NX(S/T): 1
MLLALVCLLSCLLPSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD
YEADGSTNNGIFQINSRRWCSNLTPNVPNVCRMYCSDLLNPNLKDTVICAMKITQEPQGLGY
WEAWRHHCQGKDLTEWVDGCDF</pre>

Important features:
Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homolgous region to Alpha-lactalbumin / lysozyme C proteins. amino acids 34-58 (catalytic domain), 111-132 and 66-107

AGCCGCTGCCCGGGCCGGGCGCGCGCGCGCGCACCATGAGTCCCCGCTCGTGCCTGCGTTC GCTGCGCCTCCTCGTCTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCA AGCTGTCGTCGGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAAACTCAAGGGCCTGATC CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGGCGCTGGAACTGCTCCACAC TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTG TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGCAGCAGTGGGGAGCT GGAGAAGTGCGGCTGTGACAGGACAGTGCATGGGGTCAGCCCACAGGGCTTCCAGTGGTCAG GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG GAAGGCCATCCTGACACACGCGGGTGGAATGCAAGTGCCACGGGGTGTCAGGCTCCTGTG ${\tt AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTCACGCACTGAAGGAG}$ AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACC ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG ACTTCTGTGAGCAGGACATGCGCAGCGGCGTGCTGGGCACGAGGGGGCCGCACATGCAACAAG GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCCACTGGTGCTGCTTCGTCAAGTGCCGGC AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGACCGCCTGCCCTAGCCCTGCGCCGGC AACCACCTAGTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCCACCACCTACCCCAAGA ACCAGGCAGCCAACCCAACGGCCTCCCCAAAGCCTGGGCCTTTGTGGCT GCCACTGACCAAAGGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTGGCTGCCACTGACCA CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTAT TACCACCACATGGCTACTGACCGTGTCATCGGGGAAGAGGGGGGCCTTATGGCAGGGAAAATA GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAACTCTCCAGCACACA TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG GAACAAGCAGATACCAGGTCAAGGGCACCAGGTTCATTTCAGCCCTTACATGGACAGCTAGA GTCCCACCCTAGAACCCAGCCTGCCCCAGCCTGGGAAGAGGAAACTTAACCACTCC ${\tt CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT}$ GAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCGAGTCACCTTTCACAGCACTGTTCCTC

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328</pre>

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNLE VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSAGVAFAV TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKGASSSRALM NLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTC ACCACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGCGCTGG GTGCCCTGAAGGAGGTCGGAGACTGCCACAGCTGCTCGGGGACGCAGGCGCAGCTG CAGACCACGCGCGCGGGCTTGGGGGGGGGCGCGAGCTGATGGAGCAGGAGAGCGCCCT GCGGGAACTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACTCCTGCGAGCCG TGCCCCACGTCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC GTGGGCGCGCGCAGGATCACTGCGCAGATGCCAGCGCACCTGGTGATCGTTGGGGGCC CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTCATGATGC TGCACACGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG AAAAGGCACAACTGCTGACCCCGCCCAGTGCCCTGGAGCCGCGCCCATTGCAGCATGTCGTA CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACC TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACTGGA AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAAA

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352</pre>

<subunit 1 of 1, 293 aa, 1 stop</pre>

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYSKWGGSSEEVPGGPWGRWVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA LLDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALR ELRERVTQGLAEAGRGREDVRTELFRALEAVRLQNNSCEPCPTSWLSFEGSCYFFSVPKTTW AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS HWNQGEPNDAWGRENCVMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:

Type II transmembrane domain:

amino acids 31-54

N-glycosylation sites.

amino acids _73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

GCCAGGGGAAGAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG GCAGCCCCGCCGCCGCAGCCCCTTCTCCTCTTTTCTCCCACGTCCTATCTGCCTCTCG $\tt CGCGCTCCCGCTGCCGGGTG{\color{blue} \underline{ATG}} GAAAACCCCAGCCCGGCCGCCCTGGGCAAG$ GCCCTCTGCGCTCTCCTGGCCACTCTCGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTC CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA CGGCCTTCCCCAAGCAGTACCCCCTGTTCCGCCCCCCTGCGCAGTGGTCTTCGCTGCGG GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTCAGTAACGGGCTGCG CGACTTTGCGGAGCGCGAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGGAGG CGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCCGCCGTCCCCAGCGGCACCGGGCAGACG ${\tt TCGGCGGAGCTGGAGGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCC}$ CAGCCCCGACTGGTTCGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG TCCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCCCAG CCACCCGGCCAACTCCTTCTACTACCCGCGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA ${ t AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTC}$ CCTGTGGTCGTCCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA CTCGCTACGTCCGGGTCCAGCCCGCCAACAACGGGAGCCCCTGCCCCGAGCTCGAAGAAGAG ${\tt GCTGAGTGCGTCCTGATAACTGCGTC}$ GAGCCATGGGGGTGTCGGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCACAGGG GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCCGCCGACCATCTCTGCACTGAAGGGCCCT CTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG CCCCCGTGTCCCGTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCCTTCATCG TCCAGGGGCCTGGCTCCCACGTGGTTGCAGATACCTCAGACCTGGTGCTCTAGGCTGTGCTG AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG TTTCGGAAGCGTCAGTGTTTCCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971</pre>

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALMKEIEAAGEALQSVHEVF SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYP YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP RAFIPPAPVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTKSRTRYVRVQPA NNGSPCPELEEEAECVPDNCV

Important features:

Signal peptide:

amino acids 1-26

[**]

FIGURE 88

GGCGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGCGTGA TATTGACAAACTGAAGCTTTCCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGA CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC CAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAATGGGAAGGTTTTATTGAAAACTA CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCAGAAATTTT ATCCAACTTTGTTTGGAAGCTTATTATGACAATACCATTTTTCATAGAGTTGTGCCTGGTTT CATTCAAAGATGAATTTCATTCACGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCA AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTCGAGCAGATGAACT TAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC TGTCAGAAGTAGACATTGATGACGAAAGACCACATAATCCACACAAAATAAAAGCTGT GAGGTTTTGTTTAATCCTTTTGATGACATCATTCCAAGGGGAAATTAAAAGGCTGAAAAAAGA GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTTAGTTTACTTT CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT TGTAGAAAGTGAAAAAGGTGATGCACCAGATTTAGTTGATGATGAGAGAAGATGAAAGTGCAG AGCATGATGATATTTGATGGTGATGAAAAGAACCTGATGAGAAAAGAATTGCCAAAAAA TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC AGTCAGCCGCAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAAAACGGGAACTCTTAGCAG CAAAACAAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAAGAAGTGAAGAGGAAGAA GCCCTCCAGATGGTGCTGTTGCCGAATACAGAAGAAAAGCAAAAGTATGAAGCTTTGAG GAAGCAACAGTCAAAGAAGGGAACTTCCCGGGAAGATCAGACCCTTGCACTGCAGCAGT TTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA GTAGAAGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGT GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAACAGCCATTG TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTTGTCTGGTTTTG AAAAACAATTATCTTGTTTTTGCAAATTGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGG TACATGTGTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCCT TCCACAAAAAAAAAAAAAAAAAAAAAAAAAAA

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><subunit 1 of 1, 472 aa, 1 stop

><MW: 53847, pI: 5.75, NX(S/T): 2

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VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFNPFDDIIPREIKRLKKEK
PEEEVKKLKPKGTKNFSLLSFGEEAEEEEEEVNRVSQSMKGKSKSSHDLLKDDPHLSSVPVV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKSV
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEEAPPDGAVAEYRREKQKYEALRK
QQSKKGTSREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMSHVLQFEDKSRKVK
DASMQDSDTFEIYDPRNPVNKRRREESKKLMREKKERR

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature. amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

CCCGCCTCGGCTTTGAGGCGAGAGAGTGTCCCAGACCCATTTCGCCTTGCTGACGGCGTCG AGCCCTGGCCAGAC<u>ATG</u>TCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC GTGGCCGCCGGCGGACCAGCACGGCGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAA CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTG CTCCTTCAAGTGGTTTTGGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA GGAGGAACAAATACAGGTGCCTTGCACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAAC CCTGCAAGGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCT TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAGCCCTGGAAA GGAATCAGAGATGCTACCACCTACCCGCCTGGATGGAGTCTCGCTCTGTCGCCAGGCTGGAG TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGAGTCTCCTGC $\tt CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCCT\overline{G}GGGCCAGCTGGCCTCG$ GAACGTGTACGCGCCGGCGCGCGCCCCGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCC CGGGAGGCGCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCGC GAGAAAGTGGTGCTGGTGTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGA CGACAGCCACGCGCGGGAACTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTCGGCCAGTCGGCG GGGGCCATGAGCATCTCAGGACTGATGATGTCACCCCTAGCCTCGGGTCTCTTCCATCGGGC CATTTCCCAGAGTGGCACCGCGTTATTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGG CCAAGAAGGTTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCCTCCAACT GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTG TGATCCCAGATGACCCTTTGGTGCTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCTTATAATATCACCAAGGAGCAGGT ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCAC TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGC TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC TATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGACTAGCCA TGGACATACCTGGGGACAAGAGTTCTACCCACCCCAGTTTAGAACTGCAGGAGCTCCCTGCT GCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGTTGTGTGGGACCTGCACTGCCCTTTCCAGCC TGACATCCCATGATGCCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTTCCCTTCTTCAAATCCT CCCACCCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTCGACCCAGACTGCCACTGC TCACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACTTTTGGTAGTTTGGGA TCTTCTCCCACCCACACTTATCTCCCCCAGGGCCACTCCAAAGTCTATACACAGGGGTGG TCTCTTCAATAAAGAAGTGTTGATTAGAAAAAAAAAAA

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<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

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LGILRFAPPEPPEPWKGIRDATTYPPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWFPGGAF
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRFLQLNFQRDPEEIIWSMSPVVDGVVIPDD
PLVLLTQGKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMD
IVQDATFVYATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

 ${\tt GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAG{\color{red} {\bf ATG}}{\tt CTACTGCCACTGCT}}$ GCTGTCCTCGCTGGCCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGG AGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCCGA CAAGACTGGACAGGTCTACCCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAC CAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGAGAGGTGGAAATGAGCACCCGGGGCC GATTCCAGCTCACTGGGGATCCCGCCAAGGGGAACTGCTCCTTGGTGATCAGAGACGCGCAG ATGCAGGATGAGTCACAGTACTTCTTTCGGGTGGAGAGGGAAGCTATGTGACATATAATTT CATGAACGATGGGTTCTTTCTAAAAGTAACAGTGCTCAGCTTCACGCCCAGACCCCAGGACC ACAACACCGACCTCACCTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACC GTCCGACTCCGTGTGGCCTATGCCCCCAGAGACCTTGTTATCAGCATTTCACGTGACAACAC GCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCCATACCTGGAAGCCCAAAAAGGCCAGT TCCTGCGGCTCCTCTGTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCCTGCAG AACAGAGTCCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGG GGTGAAGGCTGGGGATTCAGGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGC AGCGAGCCCTGGACCTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCAA GCAAACAGGACAGTCCTGGAAAACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCA GGGGACAGGTTCTGAGCCCCTCCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTT CAAGTGGAGCACGAAGGAGAGTTCACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCACGT CTCTCTCAGCCTCTCCGTGCACTATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAG CGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTCCTCTGCCTGGCCCTGATCATCATGAAG ATTCTACCGAAGAGACGGACTCAGACAGAAACCCCGAGGCCCAGGTTCTCCCGGCACAGCAC GATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCTGGCTCAGAAGCGGAATCAGA AAGAACCAGAAAAAGCAGTATCAGTTGCCCAGTTTCCCAGAACCCAAATCATCCACTCAAGC CCCAGAATCCCAGGAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCA GACCCAGGCCTGAGGCCCGGATGCCCAAGGGCACCCAGGCGGATTATGCAGAAGTCAAGTTC CAA<u>TGA</u>GGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAG ${ t CTCTCTTTCTCTCTTTTAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCTGTAATC}$ CCAGCACTTTGGGAGGTTGAGGTGGGCAGATCGCCTGAGGTCGGGAGTTCGAGACCAGCCTG GCCAACTTGGTGAAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCAGG CGCCTGTAATCCTACCTGGGAAGCTGAGGCAGGAGAATCACTTGAACCTGGGAGACGG AGGTTGCAGTGAGCCAAGATCACACCATTGCACGCCAGCCTGGGCAACAAAGCGAGACTCCA TCTCAAAAAAAAATCCTCCAAATGGGTTGGGTGTCTGTAATCCCAGCACTTTGGGAGGCTA AGGTGGGTGGATTGCTTGAGCCCAGGAGTTCGAGACCAGCCTGGGCAACATGGTGAAACCCC ATCTCTACAAAAATACAAAACATAGCTGGGCTTGGTGGTGTGTGCCTGTAGTCCCAGCTGT CAGACATTTAAACCAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACC TACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCCG ATCCCACCAAAACCAAGTTGGCCACGAGAGTGACCTCTGGTCGTCCTCACTGCTACACTCCT GACAGCACCATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCA AAAGGGGGAGGAATGAATAATCCACCCCTTGTTTAGCAAATAAGCAAGAAATAACCATAAAA GTGGGCAACCAGCAGCTCTAGGCGCTGCTCTTGTCTATGGAGTAGCCATTCTTTTGTTCCTT TACTTTCTTAATAAACTTGCTTTCACCTTAAAAAA

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><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

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YVTYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSL
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPR
FSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTOADYAEVKFO

Important features:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

Immunoglobulins and major histocompatibility complex proteins signature.

amino acids 365-371

 ${ t TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCA} { t ATG} { t AACTGTTATTTACTGCTGCGTTT}$ AAGTCAAGCAGCCAGTGCGATCTCATTTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA ${ t CAATGGAAACAATTCTTTCCAGTACAAGCTTTTGGGAGCTGGAAGTACTTTTATCA}$ ${\tt TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC}$ TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA GTTTGTCATCAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG TCTGGAACAACAAGTGTATTAATTAAACTTTCAGATGTTAATGACAATAAGCCTATATTTAA AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT GATTCGCAAACATTTGACATTATTACTAATCATGAAACTCAAGAAGGAATAGTTATATTAAA AAAGAAAGTGGATTTTGAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAACCATC ATGTTCCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCACTTTCATTAAGATCCAG GTGGAAGATGTTGATGAGCCTCCTCTTTTCCTCCTTCCATATTATGTATTTGAAGTTTTTGA AGAAACCCCACAGGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCAATATCAATGATAATGGTACAATC ${ t ACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC}$ AGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAACATCA ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTT TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAAGTTTTACAATCATAGATAATCAAG ATAACACAGCTGTCATTTTGACTAATAGAACTGGTTTTAACCTTCAAGAAGAACCTGTCTTC TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTTGCATTATGATCATA TTTGGGTTTATTTTTTTGACTTTGGGTTTAAAACAACGGAGAAAACAGATTCTATTTCCTGA GAAAAGTGAAGATTTCAGAGAGAATATATTCCAATATGATGATGAAGGGGGTGGAGAAGAAG ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT CGGAAAACCACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA CAGTGCCATATTCAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG $\tt CCCCTCCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCC$ CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT GCTTTTTACCATCAAAATTTTTAAAAGTGCTAATGTGTATTCGAACCCAATGGTAGTCTTAA AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC CTGGAGTAAATACTCCATGGTTATTTTAAGCTACCTACATGCTGTCATTGAACAGAGATGTG GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAAATAATG TAGGAAGATATTAAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAATTTAAAGGAGCAAAAATTTG CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCCATGAAGTATTGTTTCCTTTAT TTAAA

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GRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL
LYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSD
VNDNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYYVFEVFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
DESIEEHHFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
SLTSTNTLTIHVCDCGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESAVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518, 516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

ATTTCAAGGCCAGCCATATTTTTTTGTTGAACCAACAACAGGAGTCATAAGAATATTTTNTA
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAAACTTTCAGATGTTAATGACAA
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC
AGCATTGAAGAGAGGATGATTCGCAAACATTTGACATTATT

FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCCCCGGGCGCGCGGACCCCAACCCCGAC CCAGAGCTTCTCCAGCGGCGCGCGCGAGCAGGGCTCCCCGCCTTAACTTCCTCCGCGGGG $\tt CCCAGCCACCTTCGGGAGTCCGGGTTGCCCACCTGCAAACTCTCCGCCTTCTGCACCTGCCA$ ${\tt CCCCTGAGCCAGCGGGCCCCCGAGCGAGTC}$ $\hbox{\tt TTCATTCTCGCCTTCCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG}$ GATTTACTCCTATGCCGGCGACAACATCGTGACCGCCCAGGCCATGTACGAGGGGCTGTGGA ${\tt TGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT}$ $\tt CTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGAT$ ${\tt AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGC}$ ${\tt AGAAGATGAGGATGGCTGTCATTGGGGGGTGCGATATTTCTTCTTGCAGGTCTGGCTATTTTA}$ GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCCCAGT TTCTGGGAGGTGCCCTACTTTGCTGTTCCTGTCCCCGAAAAACAACCTCTTACCCAACACCA $\overline{\mathsf{GAGAAATCATGTTGAAACAAACCGAAAATGGACATTGAGATACTATCATTAACATTAGGAC}$ ACCCATGTGTTAAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCCTCA ATATAGGAGGGAAGATTTTTCCATTTGTATTACTGCTTCCCATTGAGTAATCATACTCAAAT GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGTATATACATGTTTTTCTATTAAAA ATAGACAGTAAAATACTATTCTCATTATGTTGATACTAGCATACTTAAAATATCTCTAAAAT TTATATACATATGTAACAGTCAAATATCATTTACTCTTCTTCATTAGCTTTGGGTGCCTTTG ${\tt CCACAAGACCTAGCCTAATTTACCAAGGATGAATTCTTTCAATTCTTCATGCGTGCCCTTTT}$ CATATACTTATTTTATTTTTACCATAATCTTATAGCACTTGCATCGTTATTAAGCCCTTAT ${\tt TTGTTTTGTGTTTCATTGGTCTCTATCTCCTGAATCTAACACATTTCATAGCCTACATTTTA}$ GTTTCTAAAGCCAAGAAGAATTTATTACAAATCAGAACTTTGGAGGCAAATCTTTCTGCATG ACCAAAGTGATAAATTCCTGTTGACCTTCCCACACAATCCCTGTACTCTGACCCATAGCACT $\tt CTTGTTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT$ AACACAACTTTATTGATTGAATTTTTAAGCTACTTATTCATAGTTTTATATCCCCCTAAACT ACCTTTTTGTTCCCCATTCCTTAATTGTATTGTTTTCCCAAGTGTAATTATCATGCGTTTTA ${\tt TATCTTCCTAATAAGGTGTGGTCTGTTTGTCTGAACAAGTGCTAGACTTTCTGGAGTGATA}$ ${\tt ATCTGGTGACAAATATTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTTT}$ ${\tt TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTAA}.$ ${ t TTAGTTTATTACTCTTATTCTTTGAACATGAACTATGCCTATGTAGTGTCTTTATTTGCT$ CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACGCTACCTTCATGTGATT CACTGCCTTCCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACACACATACCTTCAT GTGGTTCAGTGCCTTCCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACGCACATAC CTTCATGTGGCTCAGTGCCTTCCTCTCTACCAGTCTATTTCCATTCTTTCAGCTGTGTCT ${\tt GACATGTTTGTGCTCTGTTCCATTTTAACAACTGCTCTTACTTTTCCAGTCTGTACAGAATG}$ $\tt CTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTTGGCACTGGTGTCTGGAGACCTG$ GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGAGCAAGGCATTTGGCTGCTGTAA GCTTATTGCTTCATCTGTAAGCGGTGGTTTGTAATTCCTGATCTTCCCACCTCACAGTGATG ${\tt TTGTGGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAATTTAAAAAGTGCTAT}$ ACTAAGGGAAAGAATTGAGGAATTAACTGCATACGTTTTGGTGTTTGCTTTTCAAATGTTTGA AAATAAAAAAAATGTTAAG

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185</pre>

><subunit 1 of 1, 211 aa, 1 stop

>< MW: 22744, pI: 8.51, NX(S/T): 1

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Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein amino acids 119-133

GGGCCCGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTCGCAGANCACCGGGCAGATCCAGTGCAA
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGGCGCGATATTTCTT
CTTGCAGGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT
TCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC
TGGGCTGCTGCTTCTCTCTCCCTTCTGGGAGGTGCCCTACTTTGCTGTTCCTGCGA

 ${\tt TCATAGGGGGGCGCGATATTTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA} \\ {\tt TGGCAATAGAATCGTTCAAGAATTNTATGACCCTATGACCCCAGTCAATGCCAGGTACGAAT} \\ {\tt TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTACTTTGCTGTTCCTG} \\ {\tt CTTTGCTGTTCCTG} \\$

GCGTGCCGTCAGCTCGCCGGGCACCGCGCCCTCGCCCTCCGCCCCTGCGCCTGCAC ACCGGTCCCCGCCTTTTTGTAAAACTTAAAGCGGGCGCAGCATTAACGCTTCCCGCCCCGGT GACCTCTCAGGGGTCTCCCCGCCAAAGGTGCTCCGCCGCTAAGGAACATGCCGAAGGTGGAG CAGGTCCTGAGCCTCGAGCCGCAGCACGAGCTCAAATTCCGAGGTCCCTTCACCGATGTTGT CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTA CAGCACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCCTCAATT AATGTATCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT TATGGTTCAGTCTATGTTTGCTCCAACTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG CAAAACCGGAAGACCTTATGGATTCAAAACTTAGATGTGTTTTGAATTGCCAGCAGAGAAT GATAAACCACATGATGTAGAAATAAATAAATTATATCCACAACTGCATCAAAGACAGAAAC ACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAACAAGCAGTTCAAG GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTCAGCATTAGC CCCAACTGGGAAGGAGGAGGCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTGTTCTTTA TCGTTGGTGTAATTATTGGGAAGATTGCCTTGTAGAGGTAGCATGCACAGGATGGTAAATTG GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAATT AGATACACACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG ATTGAGGGGGAAAAAGAATGATCTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAAT GGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGCTGGATTACCTC TCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCCAGCAT GCTGGGGAGTGCGGTCAGCTCCACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTG CTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT TGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAA GCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACTGTTATTCAGAGATGTTTAATGCATA TTTAACTTATTTAATGTATTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGC TGCGTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTATTGGGATGCTGGAGAAGAGCTGCCA CCACCTCTCAACCATTACTCACACTTCCAGCGCCCAGGTCCAAGTCTGAGCCTGACCTCCCC TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAAACTCTTCAGCGAATCCTTCTAGTAC TAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGA CTATGTAGCATCTTGAAAAGAAAATTATAATAAAGCCCCAAAATTAAGAAAA

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<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

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Important features:

Transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT

AAATGACACCNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCCCCAGCATGCTG

GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTGCTTT

CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC

CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTTTGA

CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT

AAATTGTATTGGTTCATGTAGTGAAGTCAAACTGTTATTCAGAGATGTTAATGCATATTTA

ACTTATTTAATGTATTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG

TGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTTGGGAAGATTGCTTGTAGAGGTA
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CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT
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<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

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YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISPQHVLTAAHCVHDGKDYVKGSKKLRV
GLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGGRRRKKSGRGQRIAEGRPS
FQWTRVKNTHIPKGWARGGMGDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCSVSDESNDLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKIIAVYSG
HQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site. amino acids 165-170

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT GTGACAGCAGGCAGAGGACCTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGG ${\tt ATCCAAGC} \underline{{\tt ATG}} {\tt GAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCTTTCTGGCTTTC}$ CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC TGCCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA AGTGCCAAGCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACT GTGGTTGCACTTCCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAAGGTCCTGATCACTT ATATCTGGAAACCAAAACCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA ATGGCTGGACCACTCACAGCAGATTTCATTGTCAAGATTCGTAACTCGGGCTCCGCTGACAG CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC CTTATGACCTCTACCATCCCCTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCC TCGTGTGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCA TGTCACTTCAGTGGAAGAGTGGAAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT GGCCAGGGCCTCAGATACCGTGTGGTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGG CTGTAGCCCAAAAACAAGCCCCACATAAAAGAGGGAATGCATCGTACCCACTCCCTGCTATA AACCCAAAGAGAAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA ${\tt GAAGAAGGAGCTGTGTCAGAGGAGCCCTCG} \underline{{\tt TAA}}{\tt GTTGTAAAAGCACAGACTGTTCTATA}$ TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA AAAAAAAA

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<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

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AKGTTLVVELAPKVLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVLKGPDHLYLETKTLQGTKGENSLSSTGTFL
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFPCS
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPCTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKLPVEAKLPWFKOAOELEEGAAVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

CGGACGCGTGGGCGCGCTGCGGAACTCCCGTGGAGGGCCCGGTGGGCCCTCGGGCCTGAC GCCCGCCGGTTCGTGGGGCCCAGGGTCCAGCGGCTGCGCAGAGGCGGGGACCCCGGCCTCAT GCGCCGGTCAGCTCCGCCGAGCTCCGCCAGGCCGCGAGTGCGGCCCAGAGCCTGGCGT CAGCGGGGTGGCCGACTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA TCTGGGGCACTTTCTACTCACCAATCTTCTCCTTGGACTCCTCAAAAGTTCAGCTCCCAGCA GGATTGTGGTAGTTTCTTCCAAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC AGTGAACAAAGCTATAATAAAAGCTTTTGTTATAGCCGGAGCAAACTGGCTAACATTCTTTT TACCAGGGAACTAGCCCGCCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTG GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC GGCCTCTTCACCTGAGGTAGAAGGAGTGTCAGGAAGATACTTTGGGGATTGTAAAGAGGAAG AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACTCTGGGATATCAGTGAAGTG ATGGTTGGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAAACTGCATATCAG TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACTTGAAGAAAAAGAATTTTG ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTT GTACAATGAAAAATACAATTATATTGTAAAAATTATAACTGGGCAAGCATGGATGACATATTA ATATTTGTCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTTTGTGTGGAAATTATCTGC CTGGTGTGCACACAGTCTTACTTGGAATAAATTTACTGGTAC

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<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

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Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCC CTTTCCTAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGAC $\tt CCCAGCGTTACC\underline{\textbf{ATG}} CATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCT$ GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACAACTGAAATAACAAGTCTTGCTACAGAGA ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGT CGTTTCAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAGGAAGAATT TCCAAATGAAAATCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC AGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAG AGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAG TGACCCCATTCAAGAAATTCGGGACTTAGCAGAAATCACCACTCTTGATCGCAGCAAAAGAA ATATCATTGGATATTTTGAGCAAAAGGACTCGGACAACTATAGAGTTTTTGAACGAGTAGCG AATATTTTGCATGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAAACCGGAAAG ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACT ${\tt TGGGAGCTATGACAAATTTTGATGTGACTTACAATTTGGATTCAAGATAAATGTGTTCCTCTT}$ GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCCAGAATGAAGTAGCTCGGC AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT CCTCTTCTGCACATACAGAAAACTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTTAG GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCCTGGAAAACTCAAGCAATTCG TATTTGACTTACATTCTGGAAAACTGCACAGAGAATTCCATCATGGACCTGACCCAACTGAT ACAGCCCCAGGAGAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA ${\tt ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTT}$ AAAAACAGTTTGTAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTA

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689</pre>

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

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GQRSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKDSDNYRVFERVANILH
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI
TFENGEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCPVIAIDSFRHMYVFGDFKDVLIPGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATG GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

 $\tt GCCCACGCGTCCG{\color{blue} \underline{ATG}} GCGTTCACGTTCGCGGCCTTCTGCTACATGCTGGCGCTGCTCA$ CTGCCGCGCTCATCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGACTGAT TACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGTACTCCCAGAGTACCTCAT CCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA TGCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGA GTGCAAATTAGCTTTTTATCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTT TGGTGAGCTCT<u>TAG</u>AACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTTGCTTGTGGAAAGACTG TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT GATTACCTCTGGTGTTGACAGGTTTGAACTTGCACTTCTTAAGGAACAGCCATAATCCTCTG AATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTTTATAGGAACTTGTA GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC ${\tt TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAACTTCATGGGTTTCCTCATCTGTC}$ ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTT GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA TATACTTGCTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG TACTACAGATTTTCAAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCTTTAGT GCAATACAATAAAACTCTGAAATTAAGACTC

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<subunit 1 of 1, 144 aa, 1 stop</pre>

<MW: 16699, pI: 5.60, NX(S/T): 0

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Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCTG

AATCCCCTTGTACTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC

AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCTCTTGGCATATCATATTTGGAGGTATA

TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT

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<MW: 36223, pI: 5.06, NX(S/T): 1

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ELRQEQLMSLMPKMHLLFPLTLVRSFWSDMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEI
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Important features:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93